


```
Db      61  TATGTTGTGATGATGACCCAGACTCCACTCACTCTTTGTTCGTTTACCAATTGGACAACCAAGCTCC 120
Qy      121  ATCTTTGCAAGTCAAGTCAGAGCCCTCTTAGATAGTAGTGAAGACATATTTGAATTGG 180
Db      121  ATCTTTGCAAGTCAAGTCAGAGCCCTCTTAGATAGTAGTGAAGACATATTTGAATTGG 180
Qy      181  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 240
Db      181  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 240
Qy      241  TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 300
Db      241  TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 300
Qy      301  AGCAGAAATAGAGGCTGAGGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
Db      301  AGCAGAAATAGAGGCTGAGGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
Qy      361  CGGACGTTCCGTTGGAGGCCACCAAGCTGGAATCAAA 396
Db      361  CGGACGTTCCGTTGGAGGCCACCAAGCTGGAATCAAA 396

RESULT 2
MUSIGKCLM
LOCUS      Mouse IgMk rearranged kappa light-chain mRNA variable region
DEFINITION (V-J-kappa) anti-DNA autoantibody.
ACCESSION M20830
VERSION    M20830.1 GI:196939
KEYWORDS   V-region; autoantibody; immunoglobulin kappa-chain; immunoglobulin
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 428)
AUTHORS    Kofler,R., Strohal,R., Balderas,R.S., Johnson,M.E., Noonan,D.J.,
           Duchosal,M.A., Dixon,F.J. and Theofilopoulos,A.N.
TITLE      Immunoglobulin kappa light chain variable region gene complex
           organization and immunoglobulin genes encoding anti-DNA
           autoantibodies in lupus mice
JOURNAL    J. Clin. Invest. 82 (3), 852-860 (1988)
MEDLINE    88331394
PUBMED     3138286
COMMENT    Original source text: Mouse (strain (NZBxW)F-1) spleen hybridoma
           cell line BXW-DNA14, cDNA to mRNA.
           Draft entry and computer-readable sequence [1] kindly submitted by
           R.Kofler 28-JUL-1988.

FEATURES   Location/Qualifiers
            source             1..428
                                /organism="Mus musculus"
                                /mol_type="mRNA"
                                /db_xref="taxon:10090"
            mRNA              1..>428
                                /product="IgMk mRNA"
            CDS                33..>428
                                /note="IgMk light chain precursor"
                                /codon_start=1
                                /protein_id="AAA38844.1"
                                /db_xref="GI:196940"
                                /translations="MMSPAQFLFLVLWIRETNGDVVMTOTPLTSLVTIGOPASISCK
                                SSQSLSDSGKTYLWLLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISR
                                VEAEDLGVYICWQGTHTFPRTFGGKLEIK"
            sig_peptide        33..92
                                /note="Ig light chain signal peptide"
            mat_peptide        93..>428
                                /product="Ig light chain"
            ORIGIN              Chromosome 6.

Query Match      98.0%; Score 388; DB 10; Length 428;
Best Local Similarity 98.7%; Pred. No. 2.2e-117;
Matches 391; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1  ATGATGAGTCTCTGCCAGTTCTCTGTTCTGTAGTGTCTGGATTCTGGAAACCAACGGT 60
Db      33  ATGATGAGTCTCTGCCAGTTCTCTGTTCTGTAGTGTCTGGATTCTGGAAACCAACGGT 92
Qy      61  TATGTTGTGATGACCCAGACTCCACTCCTTTGTTCGGTTACCAATTGGACAACCAAGCTCC 120
Db      93  GATGTTGTGATGACCCAGACTCCACTCCTTTGTTCGGTTACCAATTGGACAACCAAGCTCC 152
Qy      121  ATCTTTGCAAGTCAAGTCAGAGCCCTCTTAGATAGTAGTGAAGACATATTTGAATTGG 180
Db      153  ATCTTTGCAAGTCAAGTCAGAGCCCTCTTAGATAGTAGTGAAGACATATTTGAATTGG 212
Qy      181  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 240
Db      213  TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 272
Qy      241  TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 300
Db      273  TCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 332
Qy      301  AGCAGAAATAGAGGCTGAGGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
Db      333  AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCT 392
Qy      361  CGGACGTTCCGTTGGAGGCCACCAAGCTGGAATCAAA 396
Db      393  CGGACGTTCCGTTGGAGGCCACCAAGCTGGAATCAAA 428

RESULT 3
AY571288
LOCUS      Mus musculus anti-CMV coat protein monoclonal antibody CymMV-L 23
DEFINITION immunoglobulin light chain variable region mRNA, complete cds.
ACCESSION AY571288
VERSION    AY571288.1 GI:50346341
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 930)
AUTHORS    Wang,H.L., Lee,C.H. and Hsu,H.T.
TITLE      Molecular Cloning and Sequencing of Heavy and Light Chain cDNAs
           from Papaya ringspot and Cymbidium mosaic viruses-Specific
           Monoclonal Antibodies
JOURNAL    Zhi Wu Bing Li Xue Hui Kan 13 (2004) In press
REFERENCE   2 (bases 1 to 930)
AUTHORS    Wang,H.L., Lee,C.H. and Hsu,H.T.
TITLE      Direct Submission
JOURNAL    Submitted (11-MAR-2004) Graduate Institute of Biology Science,
           National Kaohsiung Normal University, 116, Ho Ping Ird, Kaohsiung
           802, Taiwan

FEATURES   Location/Qualifiers
            source             1..930
                                /organism="Mus musculus"
                                /mol_type="mRNA"
                                /db_xref="taxon:10090"
                                /cell_line="11A12F5"
                                /cell_type="hybridoma"
            CDS                3..722
                                /note="anti-Cymbidium mosaic virus coat protein mAb
                                CymMV-L 23"
                                /codon_start=1
                                /product="anti-CMV coat protein monoclonal antibody
                                CymMV-L 23 immunoglobulin light chain variable region"
                                /protein_id="AAT74922.1"
                                /db_xref="GI:50346342"
                                /translation="MMSPAQFLFLVLWIRETNGDVVMTOTPLTSLVTIGOPASISCK
                                SSQSLSDSGKTYLWLLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISR
                                VEAEDLGIYICWQGTHTFPRTFGGKLEIKRAADAAPTIVIFPSSSEQLTSGGASVVCF
                                LNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYMSSTILTITKDEYERHNSVT
```

ORIGIN		CEATHKSTSPIVKSFNRNEC"	
Query Match		97.2%; Score 384.8; DB 10; Length 930;	
Best Local Similarity		98.2%; Pred. No. 2.7e-116;	
Matches 389; Conservative		0; Mismatches 7; Indels 0; Gaps 0;	
Qy	1	ATGATGAGTCCCTGCCAGTCCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACCGGT	60
Db	3	ATGATGAGTCCCTGCCAGTCCCTGTTCTGTTAGTCTCTGGATTCCGGAAACCAACCGGT	62
Qy	61	TATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCATTTGGACAACCAAGCCTCC	120
Db	63	GATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCATTTGGACAACCAAGCCTCC	122
Qy	121	ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATTGG	180
Db	123	ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATTGG	182
Qy	181	TTGTTACAGAGCCAGGCAGTCTCCAAAGCGCCTAATCTATCTGTTGCTTAAACTGGAC	240
Db	183	TTGTTACAGAGCCAGGCAGTCTCCAAAGCGCCTAATCTATCTGTTGCTTAAACTGGAC	242
Qy	241	TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	300
Db	243	TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	302
Qy	301	AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGCAAGGTACACATTTTCCT	360
Db	303	AGCAGATGGAGGCTGAGGATTTGGGAATTTATTATTGCTGCAAGGTACACATTTTCCT	362
Qy	361	CGGACGTTCCGTTGGAGGCACCAAGCTGGAATCAAA	396
Db	363	CGGACGTTCCGTTGGAGGCACCAAGCTGGAATCAAA	398
RESULT 4		AF045492 393 bp mRNA linear ROD 28-FEB-1998	
AF045492		Mus musculus dC3 anti-poly(dC) monoclonal antibody kappa light	
LOCUS		chain variable region, (IgK) mRNA, partial cds.	
DEFINITION		AF045492.1 GI:2906067	
ACCESSION		Mus musculus (house mouse)	
VERSION		Mus musculus	
KEYWORDS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
SOURCE		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
ORGANISM		1 (bases 1 to 393)	
REFERENCE		O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	
AUTHORS		Anti-DNA antibodies of normal mice immunized with poly(dC) are	
TITLE		structurally similar to natural autoantibodies	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 393)	
AUTHORS		O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	
TITLE		Direct Submission	
JOURNAL		Submitted (02-FEB-1998) Biochemistry, Tufts University School of	
FEATURES		Medicine, 136 Harrison Avenue, Boston, MA 02111, USA	
source		Location/Qualifiers	
		1. .393	
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6"	
		/db_xref="taxon:10090"	
		/chromosome="6"	
		/clone="dC3"	
		/cell_line="spleen cell hybridoma"	
		<1. .393	
		/gene="Igk"	
		1. .393	
		/gene="Igk"	
		/codon_start=1	
		/product="anti-poly(dC) monoclonal antibody kappa light	
gene			
CDS			
chain"		/protein_id="AAC04520.1"	
		/db_xref="GI:2906068"	
		/translation="MSPAQFLFLVLRWIRETNQGVVMTQPLTLSTVIGQPASISCKK	
		SOSLLDSNGKTYLNLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRV	
		EAGDLGVYCWQGTFFPQTFGGGTKLEIK"	
		1. .57	
sig_peptide		/gene="Igk"	
V_region		58. .357	
J_segment		/gene="Igk"	
		358. .>393	
		/gene="Igk"	
ORIGIN			
Query Match		96.0%; Score 380.2; DB 10; Length 393;	
Best Local Similarity		98.0%; Pred. No. 8.5e-115;	
Matches 385; Conservative		0; Mismatches 8; Indels 0; Gaps 0;	
Qy	4	ATGAGTCCCTGCCAGTCCCTGTTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGTTAT	63
Db	1	ATGAGTCCCTGCCAGTCCCTGTTTCTGTTAGTCTCTGGATTCCGGAAACCAACGGTGAT	60
Qy	64	GTTGTGATGACCCAGACTCCACTCCTTTGTTCGGTTACCATTTGGACAACCAAGCCTCCATC	123
Db	61	GTTGTGATGACCCAGACTCCACTCCTTTGTTCGGTTACCATTTGGACAACCAAGCCTCCATC	120
Qy	124	TCITTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGGAAGACATATTTGAATTGGTTG	183
Db	121	TCITTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGGAAGACATATTTGAATTGGTTG	180
Qy	184	TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGCTTAAACTGGACTCT	243
Db	181	TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGCTTAAACTGGACTCT	240
Qy	244	GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAAATCAGC	303
Db	241	GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAAATCAGC	300
Qy	304	AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCTCTCGG	363
Db	301	AGAGTGGAGGCTGGGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCTCTCAG	360
Qy	364	ACGTTCCGTTGGAGGCACCAAGCTGGAAAAATCAAA	396
Db	361	ACGTTCCGTTGGAGGCACCAAGCTGGAAAAATCAAA	393
RESULT 5		AF045493 393 bp mRNA linear ROD 28-FEB-1998	
AF045493		Mus musculus dC8 anti-poly(dC) monoclonal antibody kappa light	
LOCUS		chain variable region, (IgK) mRNA, partial cds.	
DEFINITION		AF045493.1 GI:2906069	
ACCESSION		Mus musculus (house mouse)	
VERSION		Mus musculus	
KEYWORDS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
SOURCE		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
ORGANISM		1 (bases 1 to 393)	
REFERENCE		O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	
AUTHORS		Anti-DNA antibodies of normal mice immunized with poly(dC) are	
TITLE		structurally similar to natural autoantibodies	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 393)	
AUTHORS		O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	
TITLE		Direct Submission	
JOURNAL		Submitted (02-FEB-1998) Biochemistry, Tufts University School of	
FEATURES		Medicine, 136 Harrison Avenue, Boston, MA 02111, USA	
source		Location/Qualifiers	
		1. .393	
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6"	
		/db_xref="taxon:10090"	
		/chromosome="6"	
		/clone="dC3"	
		/cell_line="spleen cell hybridoma"	
		<1. .393	
		/gene="Igk"	
		1. .393	
		/gene="Igk"	
		/codon_start=1	
		/product="anti-poly(dC) monoclonal antibody kappa light	
gene			
CDS			
chain"		/protein_id="AAC04520.1"	
		/db_xref="GI:2906068"	
		/translation="MSPAQFLFLVLRWIRETNQGVVMTQPLTLSTVIGQPASISCKK	
		SOSLLDSNGKTYLNLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISRV	
		EAGDLGVYCWQGTFFPQTFGGGTKLEIK"	
		1. .57	
sig_peptide		/gene="Igk"	
V_region		58. .357	
J_segment		/gene="Igk"	
		358. .>393	
		/gene="Igk"	

/strain="C57BL/6"	
/db_xref="taxon:10090"	
/chromosome="6"	
/clone="dC8"	
/cell_line="spleen cell hybridoma"	
gene	<1..>393
/gene="Igk"	
CDS	1..>393
/gene="Igk"	
/codon_start=1	
/product="anti-poly(dC) monoclonal antibody kappa light chain"	
/protein_id="AAC04521.1"	
/db_xref="GI:2906070"	
/translation="MSPAQFLFLVLVIRETNGDVVMTQPLTSLVTIGQPASISCKS	
SQSLDITNGKTYLNWLLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISR	
EADLDGIYCWQGTFFPQTGGGKLEIK"	
sig_peptide	1..57
/gene="Igk"	
V_region	58..357
/gene="Igk"	
J_segment	358..>393
/gene="Igk"	
ORIGIN	
Query Match 96.0%; Score 380.2; DB 10; Length 393;	
Best Local Similarity 98.0%; Pred. No. 8.5e-115;	
Matches 385; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
QY	4 ATGAGTCTGCCAGTTCCTGTTTCTGTAGTCTCTGGATTTCGGAAACCAACGGTTAT 63
Db	1 ATGAGTCTGCCAGTTCCTGTTTCTGTAGTCTCTGGATTTCGGAAACCAACGGTGAT 60
QY	64 GTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTTGGACAACCCAGCTCCATC 123
Db	61 GTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTTGGACAACCCAGCTCCATC 120
QY	124 TCTTGCAAGTCAAGTCAGAGCTCTTAGATAGTAGTGAAGACATATTGAAATGGTTG 183
Db	121 TCTTGCAAGTCAAGTCAGAGCTCTTAGATAGTGAAGACATATTGAAATGGTTG 180
QY	184 TTACAGAGCCAGGCAGTCTCCAAAGCCCTAATCTATCTGGTGTCTAAACTGGACTCT 243
Db	181 TTACAGAGCCAGGCAGTCTCCAAAGCCCTAATCTATCTGGTGTCTAAACTGGACTCT 240
QY	244 GGAGTCCCTGACAGGTTCACTGSCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
Db	241 GGAGTCCCTGACAGGTTCACTGSCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 300
QY	304 AGAATAGAGGCTGAGGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
Db	301 AGAGTGGAGGCTGAGGATTTGGGAATTATTATTGCTGGCAAGGTACACATTTTCTCAG 360
QY	364 ACGTTCGGTGGAGGCACCAAGCTGGAATCAAA 396
Db	361 ACGTTCGGTGGAGGCACCAAGCTGGAATCAAA 393
RESULT 6	
BC028925	
LOCUS	
BC028925 Mus musculus cDNA clone MGC:25820 IMAGE:4164906, complete cds.	
DEFINITION	
BC028925	
ACCESSION	
BC028925.1 GI:20809356	
VERSION	
MGC.	
KEYWORDS	
SOURCE	
Mus musculus (house mouse)	
ORGANISM	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 1034)	
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,	
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,	
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,	
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,	
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,	
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,	
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,	
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,	
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,	
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,	
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,	
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,	
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,	
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,	
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,	
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
Generation and initial analysis of more than 15,000 full-length	
human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
12477932	
2 (bases 1 to 1034)	
Director MGC Project.	
Direct Submission	
TITLE	
JOURNAL	
Submitted (01-MAY-2002) National Institutes of Health, Mammalian	
Gene Collection (MGC), Cancer Genomics Office, National Cancer	
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
USA	
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: Jeffrey E. Green, M.D.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Baylor College of Medicine Human Genome	
Sequencing Center	
Center code: BCM-HGSC	
Web site: http://www.hgsc.bcm.tmc.edu/cdna/	
Contact: amg@bcm.tmc.edu	
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,	
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,	
A.N., Gibbs, R.A.	
Clone distribution: MGC clone distribution information can be found	
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Series: IRAK Plate: 30 Row: m Column: 13	
This clone was selected for full length sequencing because it	
passed the following selection criteria: Hexamer frequency ORF	
analysis, Similarity but not identity to protein.	
FEATURES	
Location/Qualifiers	
1..1034	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="FVB/N"	
/db_xref="taxon:10090"	
/clone="MGC:25820 IMAGE:4164906"	
/tissue_type="Salivary gland, 10 week old female mouse"	
/clone_lib="NCI CGAP_SG2"	
/lab_host="DH10B"	
/note="Vector: pCMV-SPORT6"	
43..492	
/codon_start=1	
/product="Unknown (protein for MGC:25820)"	
/protein_id="AAH28925.2"	
/db_xref="GI:54035189"	
/translation="MMSPAQFLFLVLVIRETNGDVVMTQTPLTSLVTIGQPASISCK	
SSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTFLKISR	
VEAEDLGVIYCWQGTFFPGRSVEAPSWKSNGLMLHLQLYPSSHHPVSS"	
ORIGIN	
Query Match 94.5%; Score 374.4; DB 10; Length 1034;	
Best Local Similarity 98.2%; Pred. No. 7.8e-113;	
Matches 389; Conservative 0; Mismatches 6; Indels 1; Gaps 1;	
QY	1 ATGATGAGTCTGCTGCCAGTTCCTGTTTCTGTAGTCTCTGGATTCCTGGAACCAACCGGT 60

||||| 181 TTACAGAGCCAGCCAGTCTCCAAAGCGCCTAATCTATCTGGTCTAAACTGGACTCT 240

QY 244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATCAGC 303

Db 241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACGAGTTTACACTGAAATCAGC 300

QY 304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363

Db 301 AGAGTGGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCTCAG 360

QY 364 ACCTTCGGTGGAGGCACCAAGCTGGAATCAAA 396

Db 361 ACCTTCGGTGGAGGCACCAAGCTGGAATCAAA 393

RESULT 9

MUSILC

LOCUS 927 bp mRNA linear ROD 04-FEB-2003

DEFINITION Mus sp. mRNA for immunoglobulin light chain, complete cds, monoclonal antibody to potato virus Y coat protein.

ACCESSION D17386

VERSION D17386.1 GI:688418

KEYWORDS

SOURCE Mus sp.

ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 927)

AUTHORS Ohshima,K., Matsuura,A., Nakaya,T., Shikata,E., Kikuchi,K. and Kimura,I.

TITLE Molecular cloning and nucleotide sequences of heavy and light chain genes of a monoclonal antibody to potato virus Y coat protein

JOURNAL Ann. Phytopathol. Soc. Jpn. 60, 600-607 (1994)

REFERENCE 2 (bases 1 to 927)

AUTHORS Ohshima,K.

JOURNAL Submitted (09-AUG-1993) Kazusato Ohshima, Faculty of Agriculture, Saga University, Laboratory of Plant Virology; 1 Honjo-machi, Saga, Saga 840, Japan (Tel:81-952-24-5191(ex.2730), Fax:81-952-22-6274)

FEATURES

source location/Qualifiers

1. .927

/organism="Mus sp."

/mol_type="mRNA"

/db_xref="taxon:10095"

/note="42C07 monoclonal antibody-secreting hybridoma"

1. .720

/note="IgG3 kappa chain to potato virus Y coat protein"

/codon_start=1

/product="immunoglobulin light chain"

/protein_id="BAA04204.1"

/db_xref="GI:1794158"

/translation="WMSPAQLFLLLVCIRETNGDVVMTQTPLTSLVTIGQPASISCK SQSLLVSDGKTYLNLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGDTFTLKISR VEAEDLGVYVCWQGFTHFFTFGSGTKLEIKRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGNVLSWTDQDSKDYMSSTLSLTKEYERHNSYT CEATHKTSSTSPIVKSFNRNEC"

sig_peptide 1. .60

v_region 61. .399

c_region 400. .717

polya_signal 905. .910

polya_site 927

ORIGIN

Query Match 92.3%; Score 365.6; DB 10; Length 927;

Best Local Similarity 95.2%; Pred. No. 6.5e-110;

Matches 377; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTTAGTGTCTGGAATCGGGAAACCAACGGT 60

Db 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTTAGTGTCTGGAATCGGGAAACCAACGGT 60

QY 61 TATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCAATTGGACAACCAAGCCTCC 120

Db 61 GATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCAATTGGACAACCAAGCCTCC 120

QY 121 ATCTCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATATTTGAATTGG 180

Db 121 ATCTCTTGAAGTCAAGTCAGAGCCTCTTAGTGTAGTGTGAAAGACATATTTGAATTGG 180

QY 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 240

Db 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTCTAAACTGGAC 240

QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTCACTGAAAATC 300

Db 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTCACTGAAAATC 300

QY 301 AGCAGAAATAGAGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCTCT 360

Db 301 AGCAGAGTGGAGCTGAGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCA 360

QY 361 CGGACGTTCCGTTGGAGGCCACCAAGCTGGAATCAAA 396

Db 361 TTCACGTTCCGTTCCGGGACAAAAGTTGGAATAAAA 396

RESULT 10

MUSIGMVA

LOCUS 423 bp mRNA linear ROD 19-APR-1994

DEFINITION Mouse immunoglobulin light chain variable region.

ACCESSION L26541

VERSION L26541.1 GI:473478

KEYWORDS V-region; immunoglobulin; light chain.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 423)

AUTHORS Weiner,G.J. and Kaminski,M.S.

TITLE Anti-idiotypic antibodies recognizing stable epitopes limit the emergence of idiotype variants in a murine B cell lymphoma

JOURNAL J. Immunol. 144 (6), 2436-2445 (1990)

MEDLINE 90187894

PUBMED 1690244

REFERENCE 2 (bases 1 to 423)

AUTHORS Weiner,G.J. and Hillstrom,J.R.

TITLE Bispecific anti-idiotypic/anti-CD3 antibody therapy of murine B cell lymphoma

JOURNAL J. Immunol. 147 (11), 4035-4044 (1991)

MEDLINE 92043796

PUBMED 1834746

REFERENCE 3 (bases 1 to 423)

AUTHORS Weiner,G.J., Kostelny,S.A., Hillstrom,J.R., Cole,M.S., Link,B.K., Wang,S.L. and Tso,J.Y.

TITLE The role of T cell activation in anti-CD3 x antitumor bispecific antibody therapy

JOURNAL J. Immunol. 152 (5), 2385-2392 (1994)

MEDLINE 94179820

PUBMED 8133049

COMMENT Original source text: Mus musculus (individual isolate MS9A6) female cDNA to mRNA.

FEATURES

source location/Qualifiers

1. .423

/organism="Mus musculus"

/mol_type="mRNA"

/isolate="MS9A6"

/db_xref="taxon:10090"

/sex="female"

/cell_line="T3C"

/cell_type="B-cell"

1. .27

sig_peptide 28. .87

v_region 88. .423

ORIGIN /note="Ig light chain"

Query Match 91.5%; Score 362.4; DB 10; Length 423;
Best Local Similarity 94.7%; Pred. No. 7e-109;
Matches 375; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCAGTCTGCCAGTTCCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 60
DB 28 ATGATAAGTCTGCCAGTTCCTGTTCTCTGTTAGTCTCTGGATTCCGGAAACCAACGGT 87

QY 61 TATGTTGATGACCCAGACTCCACTCCTTTGTCGGTTACCAATTGGACAACCAAGCTCC 120
DB 88 GATGTTGATGACCCAGACTCCGCTCACTTTGTCGGTTACCAATTGGACAACCCGCTCC 147

QY 121 ATCTCTGCAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTGGAATTGG 180
DB 148 ATCTCTGCAAGTCAAGTCAGAGCTCTTAGAGGGTGTGATGGAAGACATATTGGAATTGG 207

QY 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC 240
DB 208 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC 267

QY 241 TCTGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300
DB 268 TCTGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 327

QY 301 AGCAGATAGAGGCTGAGATTTGGACTTTATTATTGCTGGCAAGTACACATTTTCTCT 360
DB 328 AGCAGATGAGGCTGAGATTTGGAAATTTATTATTGCTGGCAAGTACACATTTTCTCT 387

QY 361 CGGACGTTCCGTTGGAGGACCAAGCTGGAATCAAA 396
DB 388 CTCACGTTCCGGGCTGGACAAAGCTGGAGCTGAAA 423

RESULT 11
AR452630
LOCUS AR452630 393 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 16 from patent US 6677436.
ACCESSION AR452630
VERSION AR452630.1 GI:42684511
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Sato,K., Adachi,H. and Yabuta,N.
TITLE Humanized antibody against human tissue factor (TF) and process of production of the humanized antibody
JOURNAL Patent: US 6677436-A 16 13-JAN-2004;
FEATURES
source Location/Qualifiers
1..393
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 91.2%; Score 361; DB 6; Length 393;
Best Local Similarity 94.9%; Pred. No. 2e-108;
Matches 373; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGAAACCAACGGTTAT 63
DB 1 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATATCAACGGTGAT 60

QY 64 GTTGTGATGACCCAGACTCCACTCCTTTGTCGGTTACCAATTGGACAACCAAGCTCCATC 123
DB 61 GTTGTGATGACCCAGACTCCACTCCTTTGTCGGTTACCAATTGGACAACCAAGCTCCGTC 120

QY 124 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTGGAATTGGTTG 183
DB 121 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTGGAATTGGTTG 180

QY 184 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCT 243
DB 181 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCT 240

QY 244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
DB 241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 300

QY 304 AGAATAGAGGCTGAGGATTTGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
DB 301 AGAGTGGAGGCTGAGGATTTGGAGTTTATTATTGTTGGCAAGATACACATTTTCTCGGAC 360

QY 364 ACGTTCCGTTGGAGGCCAAAGCTGGAATCAAA 396
DB 361 ACGTTCGGAGGGGGACCAAGCTGGAATCAAAA 393

RESULT 13
AF157686

QY 184 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCT 243
DB 181 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTGATCTATCTGTGTCTAAACTGGACTCT 240

QY 244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
DB 241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 300

QY 304 AGAATAGAGGCTGAGGATTTGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
DB 301 AGAGTGGAGGCTGAGGATTTGGAGTTTATTATTGTTGGCAAGATACACATTTTCTCGGAC 360

QY 364 ACGTTCCGTTGGAGGCCAAAGCTGGAATCAAA 396
DB 361 ACGTTCGGAGGGGGACCAAGCTGGAATCAAAA 393

RESULT 12
AR452631
LOCUS AR452631 393 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 17 from patent US 6677436.
ACCESSION AR452631
VERSION AR452631.1 GI:42684512
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 393)
AUTHORS Sato,K., Adachi,H. and Yabuta,N.
TITLE Humanized antibody against human tissue factor (TF) and process of production of the humanized antibody
JOURNAL Patent: US 6677436-A 17 13-JAN-2004;
FEATURES
source Location/Qualifiers
1..393
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 91.2%; Score 361; DB 6; Length 393;
Best Local Similarity 94.9%; Pred. No. 2e-108;
Matches 373; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGAAACCAACGGTTAT 63
DB 1 ATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGGATATCAACGGTGAT 60

QY 64 GTTGTGATGACCCAGACTCCACTCCTTTGTCGGTTACCAATTGGACAACCAAGCTCCATC 123
DB 61 GTTGTGATGACCCAGACTCCACTCCTTTGTCGGTTACCAATTGGACAACCAAGCTCCGTC 120

QY 124 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTGGAATTGGTTG 183
DB 121 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGGAAGACATATTGGAATTGGTTG 180

QY 184 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCT 243
DB 181 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCT 240

QY 244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
DB 241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 300

QY 304 AGAATAGAGGCTGAGGATTTGGACTTTTATTATTGCTGGCAAGGTACACATTTTCTCGG 363
DB 301 AGAGTGGAGGCTGAGGATTTGGAGTTTATTATTGTTGGCAAGATACACATTTTCTCGGAC 360

QY 364 ACGTTCCGTTGGAGGCCAAAGCTGGAATCAAA 396
DB 361 ACGTTCGGAGGGGGACCAAGCTGGAATCAAAA 393

RESULT 13
AF157686

LOCUS	AF157686	396 bp	mRNA	linear	ROD 30-MAY-2000
DEFINITION	Mus musculus immunoglobulin kappa light chain variable region mRNA, partial cds.				
ACCESSION	AF157686				
VERSION	AF157686.1	GI:5306067			
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 396)				
AUTHORS	Park,O.Y., Jin,Y.H., Lee,M., Shin,H.J., Kim,H.I., Cho,H., Yun,C.W., Youn,J.K. and Park,S.				
TITLE	Characterization and gene cloning of monoclonal antibody specific for the hepatitis B virus X protein				
JOURNAL	Hybridoma 19 (1), 73-80 (2000)				
MEDLINE	20229330				
PUBMED	10768843				
REFERENCE	2 (bases 1 to 396)				
AUTHORS	Park,O.Y., Jin,Y.H., Lee,M., Kim,H.I., Youn,J.K. and Park,S.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JUN-1999) Microbiology, Ajou Univ. School of Medicine, Paldalku, Suwon, Keyngkido 441-749, South Korea				
FEATURES	Location/Qualifiers				
source	1..396				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="Balb/c"				
	/db_xref="taxon:10090"				
	1..>396				
	/note="anti-HBx antibody"				
	/codon_start=1				
	/product="immunoglobulin kappa light chain variable region"				
	/protein_id="AAD41897.1"				
	/db_xref="GI:5306068"				
	/translation="MSPAQFLFLVLWIRETSQDVMTQPTLTSVTIGQPASISCKS				
	SQSLDSDGETYLNWLLQRPQSPKRLIYMSKLDGVPDRFTGSGGDTFLKISR				
	EABDLGVYCYWQGHFPFTFGSGTKLEIKR"				
ORIGIN					
Query Match	90.8%; Score 359.4; DB 10; Length 396;				
Best Local Similarity	94.7%; Pred. No. 6.9e-108;				
Matches	372; Conservative 0; Mismatches 21; Indels 0; Gaps 0;				
QY	4	ATGAGTCTGCCCCAGTTCCTGTTCTGTAGTGTCTGTGATTCGGGAAACCAACGGTTAT	63		
Db	1	ATGAGTCTGCCCCAGTTCCTGTTCTGTAGTGTCTGTGATTCGGGAAACCAACGGTGTAT	60		
QY	64	GTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACAACCGCTCCATC	123		
Db	61	GTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACAACCGCTCCATC	120		
QY	124	TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAATGGAAGACATATTTGAATTGGTTG	183		
Db	121	TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAATGGAAGACATATTTGAATTGGTTG	180		
QY	184	TTACAGAGGCGAGGCAGTCTCCAAAGCGCCTAATCTATCTGTTGTCTAACTGGACTCT	243		
Db	181	TTACAGAGGCGAGGCAGTCTCCAAAGCGCCTAATTTATATGGTGTCTAACTGGACTCT	240		
QY	244	GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATCAGC	303		
Db	241	GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATCAGC	300		
QY	304	AGAAATAGAGGCTGAGGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCCCTCGG	363		
Db	301	AGAGTGGAGGCTGAGGATTTGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCATTC	360		
QY	364	ACGTTCCGTTGGAGGACCAAGCTGGAATCAAA	396		
Db	361	ACGTTCCGTTCCGGGACAAAGTTGGAATAAAA	393		

RESULT 14					
MMIGKEAD					
LOCUS	Mus musculus encoding immunoglobulin kappa light chain.				
DEFINITION	Mus musculus encoding immunoglobulin kappa light chain.				
ACCESSION	Z17401				
VERSION	Z17401.1 GI:52148				
KEYWORDS	immunoglobulin; immunoglobulin kappa light chain.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 408)				
AUTHORS	Medina,C.A. and Teale,J.M.				
TITLE	Restricted kappa chain expression in early ontogeny: biased utilization of V kappa exons and preferential V kappa-J kappa recombination				
JOURNAL	J. Exp. Med. 177 (5), 1317-1330 (1993)				
MEDLINE	93240113				
PUBMED	8478611				
REFERENCE	2 (bases 1 to 408)				
AUTHORS	Medina,C.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-OCT-1992) Medina C. A., University of Texas Health Science Center at San Antonio, Microbiology, 7703 Floyd Curl Dr., San Antonio, TX, USA, 78284				
FEATURES	Location/Qualifiers				
source	1..408				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="BALB/c"				
	/db_xref="taxon:10090"				
	/chromosome="6"				
	/clone="FL-31"				
	/cell_type="B-cell"				
	/tissue_type="Liver"				
	/dev_stage="Fetus"				
misc_feature	13..69	/product="ig kappa light chain; leader exon"			
		/citation=[1]			
misc_feature	70..408	/product="ig kappa light chain; Vk1-Jk2 region"			
		/citation=[1]			
misc_feature	70..372	/product="ig kappa light chain; Vk1 exon"			
		/citation=[1]			
misc_feature	371..372	/product="Vk1 region end/Jk2 start"			
		/citation=[1]			
misc_feature	373..408	/product="ig kappa light chain; Jk2 exon"			
		/citation=[1]			
ORIGIN					
Query Match	90.7%; Score 359.2; DB 10; Length 408;				
Best Local Similarity	94.2%; Pred. No. 8.1e-108;				
Matches	373; Conservative 0; Mismatches 23; Indels 0; Gaps 0;				
QY	1	ATGATGAGTCTGCCAGTTCCTGTTCTGTGTAGTGTCTGTGATTCGGGAAACCAACGGT	60		
Db	13	ATGATGAGTCTGCCAGTTCCTGTTCTGTGTAGTGTCTGTGATTCAGGAAACCAACGGT	72		
QY	61	TATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACAACCGCTCC	120		
Db	73	GATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACAACCGCTCT	132		
QY	121	ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAATGGAAGACATATTTGAATTGG	180		
Db	133	ATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAACCACTATTTGAATTGG	192		
QY	181	TTGTTACAGAGGCGGCGAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC	240		
Db	193	TTATTACAGAGGCGGCGAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC	252		

Qy	241	TCTGGAGTCCCTGACAGGTTCACTGCGAGTGGATCAGGACAGATTTTACACTGAAATC	300
Db	253	TCTGGAGTCCCTGACAGGTTCACTGCGAGTGGATCAGGACAGATTTTACACTGAAATC	312
Qy	301	AGCAGATAGAGGCTGAGATTTGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT	360
Db	313	AGCAGATGGAGCTGAGATTTGGAGTTATTACTGCGTGAAGGTACACATTTTCOG	372
Qy	361	CGGACGTTCCGTCGAGGACCAAGCTGGAATCAA	396
Db	373	TACACGTTCCGAGGGGGACCAAGCTGGAATAAAA	408
RESULT 15			
BC031498			
LOCUS	BC031498	1008 bp	mRNA linear ROD 13-FEB-2004
DEFINITION	Mus musculus cDNA clone MGC:27817 IMAGE:3482714, complete cds.		
ACCESSION	BC031498		
VERSION	BC031498.1	GI:21594507	
KEYWORDS	MGC.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1008)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Grimwood, J., Schmutz, J., Myers, R.M., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1008)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulaseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
Qy	1	ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAAACCAACGGT	60
Db	16	ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAAATCAACGGT	75
Qy	61	TATGTTGTGATGACCCAGACTCCACTCATTGTGCGTTACCATTTGGCAACCAAGCTCC	120
Db	76	GATGTTGTGATGACCCAGACTCCACTCATTGTGCGTTACCATTTGGCAACCAAGCTCC	135
Qy	121	ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATGG	180
Db	136	ATCTCTTGAAGTCAAGTCAGAGCTCTTTTATATACTAATGGAATAATGTTGAGTTGG	195
Qy	181	TTGTTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGAC	240
Db	196	TTATTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTCTCTGGTGTCTAACTGGAC	255
Qy	241	TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	300
Db	256	TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	315
Qy	301	AGCAGATAGAGGCTGAGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT	360
Db	316	AGCAGATGGAGGCTGAGATTTGGGAGTTATTACTGCTTGACAGATACACATTTTCOG	375
Qy	361	CGGACGTTCCGTCGAGGACCAAGCTGGAATCAA	396
Db	376	TACACGTTCCGAGGGGGACCAAGCTGGAGATAAAA	411
Search completed: September 26, 2005, 05:47:58			
Job time : 2331 secs			

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES
source
Location/Qualifiers
1..1008
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="MGC:27817 IMAGE:3482714"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
/clone_lib="NCI CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
16..735
/codon_start=1
/product="Unknown (protein for MGC:27817)"
/protein_id="AAH31498.1"
/db_xref="GI:21594508"
/translation="MMSPAQFLFLVLSIQEINGDVMTQTPLTSLVTIGQPASISCK
VSSQLFYTNKMYLSWLLQRPQSPKRLISLVSKLSDVPRFSGSGSTDFTLKISR
VEADLGVYICLQSTHPYTFGGGTGKLEIKRADAAPTVIFPPSSEQLTSGGASVVC
LNFPYKIDINVKWIKIDGSRQGVLSWTDQDSKSTYSMSSTLTLTKDEYERHNSYT
CEATHKTSTSPIVKSFNRNEC"
misc_feature
106..411
/note="IGV; Region: Immunoglobulin domain variable region
(v) subfamily"
misc_feature
418..720
/note="IGC; Region: Immunoglobulin domain constant region
subfamily"
/db_xref="CDD:cd00098"

ORIGIN
Query Match 85.9%; Score 340; DB 10; Length 1008;
Best Local Similarity 91.2%; Pred. No. 2.1e-101;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy 1 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAAACCAACGGT 60
Db 16 ATGATGAGTCTGCCAGTTCCTGTTCTGTTAGTCTCTGATTCGGGAAATCAACGGT 75
Qy 61 TATGTTGTGATGACCCAGACTCCACTCATTGTGCGTTACCATTTGGCAACCAAGCTCC 120
Db 76 GATGTTGTGATGACCCAGACTCCACTCATTGTGCGTTACCATTTGGCAACCAAGCTCC 135
Qy 121 ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATGG 180
Db 136 ATCTCTTGAAGTCAAGTCAGAGCTCTTTTATATACTAATGGAATAATGTTGAGTTGG 195
Qy 181 TTGTTTACAGAGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGAC 240
Db 196 TTATTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTCTCTGGTGTCTAACTGGAC 255
Qy 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
Db 256 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 315
Qy 301 AGCAGATAGAGGCTGAGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
Db 316 AGCAGATGGAGGCTGAGATTTGGGAGTTATTACTGCTTGACAGATACACATTTTCOG 375
Qy 361 CGGACGTTCCGTCGAGGACCAAGCTGGAATCAA 396
Db 376 TACACGTTCCGAGGGGGACCAAGCTGGAGATAAAA 411

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 05:09:16 ; Search time 86 Seconds
(without alignments)
593.632 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQTHFPRTFGGTYKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	692	100.0	132	5	ABG76923
2	692	100.0	132	8	ADR88406
3	655	94.7	238	8	ADM72033
4	653	94.4	238	8	ADP45549
5	650	93.9	135	5	ABB79729
6	644	93.1	239	6	ABP58274
7	641	92.6	132	2	AAR12361
8	641	92.6	133	8	ADO0819
9	641	92.6	133	8	ADO43845
10	640	92.5	132	5	ABG76925
11	640	92.5	132	2	ADR88409
12	639	92.3	131	2	AAR12239
13	636	91.9	132	6	ABG74244
14	630	91.0	132	5	ABG76931
15	630	91.0	132	8	ADR88415
16	628	90.8	132	2	AAR24712
17	606	87.6	142	4	AAE07032
18	606	87.6	142	8	ADQ89324
19	595	86.0	239	2	AAR24811
20	589	85.1	239	7	ADD47025
21	573	82.8	113	8	ADQ76076
22	571	82.5	113	4	AAE03751
23	571	82.5	113	8	ADQ76088
24	571	82.5	218	4	AAE03756
25	570	82.4	113	8	ADQ76078

26	569	82.2	113	8	ADQ76082	Adq76082 Heterorec
27	569	82.2	113	8	ADQ76086	Adq76086 Heterorec
28	568	82.1	112	8	ADQ76094	Adq76094 Heterorec
29	568	82.1	113	8	ADQ76092	Adq76092 Heterorec
30	568	82.1	113	8	ADQ76080	Adq76080 Heterorec
31	566	81.8	113	8	ADG25828	Adg25828 Anti-CD30
32	566	81.8	113	8	ADQ76090	Adq76090 Heterorec
33	566	81.8	114	8	ADG25839	Adg25839 Anti-CD30
34	563	81.4	112	8	ADQ76074	Adq76074 Heterorec
35	562	81.2	113	8	ADQ76084	Adq76084 Heterorec
36	562	81.2	353	2	AAV06273	Aay06273 Anti Fc a
37	560	80.9	112	4	AAE06946	Aae06946 Murine 1D
38	560	80.9	112	4	AAU09918	Aau09918 Murine mA
39	560	80.9	112	5	ABG75527	Abg75527 Mouse mAb
40	560	80.9	112	5	ADF98231	Adf98231 Murine mA
41	560	80.9	112	7	ABR61865	AbR61865 Mouse MAb
42	560	80.9	112	8	ADQ31246	Adq31246 Murine 1A
43	560	80.9	112	8	ADQ89231	Adq89231 Mouse imm
44	560	80.9	122	8	ADJ95990	Adj95990 Immunoglo
45	560	80.9	130	8	ADJ95992	Adj95992 Immunoglo

ALIGNMENTS

RESULT 1
ABG76923
ID ABG76923 standard; protein; 132 AA.

XX AC ABG76923;
XX DT 05-NOV-2002 (first entry)
XX DE Mouse 3D6 VL protein.
XX KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW notropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX OS Mus musculus.
XX PN WO200246237-A2.
XX PD 13-JUN-2002.
XX PF 06-DEC-2001; 2001WO-US046587.
XX PR 06-DEC-2000; 2000US-0251892P.
XX PA (NEUR-) NEURALAB LTD.
XX PA (AMHP) WYETH.
XX PI Basi G, Saldanha J, Yednock T;
XX DR WPI; 2002-519658/55.
XX DR N-PSDB; ABS59426.
XX PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX PS Claim 67; Fig 1; 171pp; English.
XX CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful

CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
Dd |||||
1 MMSPAQFLFLVLWIRETNGYVVMVTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIRAEADLGLYYCQGTFFP 120
Dd |||||
61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIRAEADLGLYYCQGTFFP 120

QY 121 RTFGGKLEIK 132
Dd |||||
121 RTFGGKLEIK 132

RESULT 2
ADR88406
ID ADR88406 standard; protein; 132 AA.
XX
AC ADR88406;
XX
DT 16-DEC-2004 (first entry)
XX
DE Murine 3D6 immunoglobulin light chain variable region SEQ ID NO:2.

XX 3D6; light chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; neurotropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.

XX Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal peptide
FT Protein 21..132
FT /label= mature protein
XX
PN WO2004080419-A2.
XX
XX 23-SEP-2004.
XX
PF 12-MAR-2004; 2004WO-US007503.
XX
PR 12-MAR-2003; 2003US-00388389.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha JW, Yednock T;
XX
XX WPI; 2004-668880/65.
DR N-PSDB; ADR88405.
XX

XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX
PS Claim 1; SEQ ID NO 2; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable

CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 3D6
CC immunoglobulin light chain variable region.

XX Sequence 132 AA;

Query Match 100.0%; Score 692; DB 8; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
Dd |||||
1 MMSPAQFLFLVLWIRETNGYVVMVTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIRAEADLGLYYCQGTFFP 120
Dd |||||
61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIRAEADLGLYYCQGTFFP 120

QY 121 RTFGGKLEIK 132
Dd |||||
121 RTFGGKLEIK 132

RESULT 3
ADM72033
ID ADM72033 standard; protein; 238 AA.
XX
AC ADM72033;
XX
DT 03-JUN-2004 (first entry)
XX
DE Chimeric mouse-human antibody M3C11 light chain.
XX
KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW cytotostatic; M3C11.
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX WO2004022739-A1.
PN
XX 18-MAR-2004.
PD
XX 04-SEP-2003; 2003WO-JP011318.
PF
XX 04-SEP-2002; 2002WO-JP008999.
PR
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
PI WPI; 2004-269573/25.
XX N-PSDB; ADM72032.
DR
XX Antibody against the N terminus of glypican 3(GPC3) causes cell
PT disruption and is useful as an anticancer agent.
PT
XX

PS Example 4; SEQ ID NO 18; 122pp; Japanese.

XX The invention relates to an antibody against the N terminus of glypican 3

CC (GPC3). The antibody can be used for causing cell disruption and can be

CC uses as an anti-cancer agent. The present sequence represents a chimeric

CC mouse-human antibody M3C11 light chain.

XX

SQ Sequence 238 AA;

Query Match 94.7%; Score 655; DB 8; Length 238;

Best Local Similarity 94.7%; Pred. No. 2.8e-51;

Matches 124; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 61

Db 1 MSPAQFLFLVLWIRETNGDVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 60

Qy 62 LQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPR 121

Db 61 LQRPQSPKRLIYLVSKLDGAPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPL 120

Qy 122 TFGGTKLEIK 132

Db 121 TFGAGTKLEIK 131

RESULT 4

ADP45549

ID ADP45549 standard; protein; 238 AA.

XX

AC ADP45549;

XX

DT 09-SEP-2004 (first entry)

XX

DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW mouse; antibody.

XX

OS Mus musculus.

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

XX WPI; 2004-468818/44.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-

PT D20 or NogoA623-640, useful in preparing a composition for treating CNS

PT injury or neurodegenerative disorders.

XX

PS Claim 9; SEQ ID NO 3; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human

CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a

CC dissociation constant of less than 100nM. Also described: (1) a

CC polynucleotide encoding the binding molecule; (2) an expression vector or

CC system comprising the polynucleotide; (3) a host cell comprising the

CC expression system; (4) a pharmaceutical composition comprising the

CC binding molecule and a carrier or diluent; and (5) treating diseases

CC associated with nerve repair. The binding molecule has neuroprotective

CC activity, and can be used in gene therapy. The binding molecule is useful

CC in preparing a composition for treating central nervous system (CNS)

CC injury or neurodegenerative disorders. The present sequence represents a

CC mouse binding molecule 11C7 light chain, which is used in the

CC exemplification of the present invention.

XX

SQ Sequence 238 AA;

Query Match 94.4%; Score 653; DB 8; Length 238;

Best Local Similarity 93.9%; Pred. No. 4.2e-51;

Matches 123; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 61

Db 1 MSPAQFLFLVLWIRETSGDVLTTQTPLTSLITIGQPASISCKSSQSLHSDGKTYLNL 60

Qy 62 LQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPR 121

Db 61 LQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPQ 120

Qy 122 TFGGTKLEIK 132

Db 121 TFGGTKLEIK 131

RESULT 5

ABB79729

ID ABB79729 standard; protein; 135 AA.

XX

AC ABB79729;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;

KW antibody; anticaries; transgenic plant; transgenic animal; caries;

KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

XX WPI; 2002-565838/60.

DR N-PSDB; ABN84610.

XX

PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX

PS Claim 13; Fig 3A; 30pp; English.

XX

CC The present sequence is the protein sequence of the light chain variable

CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds

CC specifically to the surface antigens of cariogenic type c Streptococcus

CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC

CC HB 12558) hybridoma cells. In an example from the invention, chimeric

monoclonal antibody TEFE was produced comprising SWA3 variable regions and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental caries in humans. The antibodies engage the effector apparatus of the human immune system when they bind cariogenic organisms, resulting in their destruction. The chimeric antibodies may be produced in edible plants, in transgenic animals, or in chicken eggs for oral ingestion

Sequence 135 AA;

WPI; 2003-103835/18.
N-PSDB; ABZ24632, ABZ24634.

New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.

Disclosure; Page 12-13; 54pp; English.

The present sequence is that of a preferred light chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field)

Sequence 239 AA;

KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.

OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1. .20
FT /label= signal peptide
FT Protein 21. .132
FT /label= mature protein

XX WO2004080419-A2.
XX
XX 23-SEP-2004.
XX
XX 12-MAR-2004; 2004WO-US007503.
XX
XX 12-MAR-2003; 2003US-00388389.
XX
XX (NEUR-) NEURALAB LTD.
XX (AMHP) WYETH.

XX Basi G, Saldanha JW, Yednock T;
XX WPI; 2004-668880/65.

XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.

XX Claim 54; SEQ ID NO 5; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and nootropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents a humanised
CC immunoglobulin of the invention.

XX Sequence 132 AA;

Query Match 92.5%; Score 640; DB 8; Length 132;
Best Local Similarity 90.2%; Pred. No. 3.3e-50;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEAEDGLYYCWGTHFP 120
DB 61 LLQKPGQSPQRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEAEDGVYYCWGTHFP 120

QY 121 RTFGGQGTKLEIK 132
|||||

Db 121 RTFGGQGTKVEIK 132
RESULT 12
AAR12239
ID AAR12239 standard; protein; 131 AA.
XX
AC AAR12239;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1991 (first entry)
XX
DE Mouse MAb 4D12 L chain V region.
XX
KW HIV-1; chimera.
XX
OS Mus sp.
XX
PN WO9107494-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433703.
XX
PR 13-NOV-1989; 89US-00433703.
XX
PA (XOMA) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
PA (ZOMA-) ZOMA CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX WPI; 1991-178106/24.
DR N-PSDB; AAQ12019.
XX
PT New chimeric mouse human antibodies - used in treatment, diagnosis and
XX prophylaxis of HIV infections.
XX Disclosure; Fig 18; 108pp; English.
XX
CC The mouse VL gene product may be used to produce chimeric mouse- human
CC Abs against HIV-1 comprising human Ig constant regions and murine
CC variable regions. These novel sequence are useful in treatment, diagnosis
CC and prophylaxis of HIV infections, and may be produced by a bacterial,
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 131 AA;

Query Match 92.3%; Score 639; DB 2; Length 131;
Best Local Similarity 91.6%; Pred. No. 4e-50;
Matches 120; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
DB 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEAEDGLYYCWGTHFP 120
DB 61 FLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEAEDLVYYCWGSHFP 120
QY 121 RTFGGQTKLEI 131
DB 121 ITFGAGTKLEL 131
RESULT 13
ABG74244
ID ABG74244 standard; protein; 132 AA.
XX
AC ABG74244;
XX
DT 22-APR-2003 (first entry)

DT 16-DEC-2004 (first entry)
DE Humanised 3D6 immunoglobulin light chain variable region SEQ ID NO:11.
XX
KW 3D6; light chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= signal peptide
FT Protein 21..132
FT /label= mature protein
XX
XX WO2004080419-A2.
XX
XX 23-SEP-2004.
XX
XX 12-MAR-2004; 2004WO-US007503.
XX
XX 12-MAR-2003; 2003US-00388389.
XX (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
XX Basi G, Saldanha JW, Yednock T;
PI WPI; 2004-668880/65.
DR
XX
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX
XX Claim 55; SEQ ID NO 11; 176pp; English.
XX
XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and nootropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents a humanised
CC immunoglobulin of the invention.
XX
SQ Sequence 132 AA;

Query Match 91.0%; Score 630; DB 8; Length 132;
Best Local Similarity 89.4%; Pred. No. 2.7e-49;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGVYVNTQTPLTSLVIGQPASISCKSSQSLDSDGKTYLNW 60
DB 1 MMSPAQFLFLVLWIRETNGVYVNTQSPSLPVTGPEPASISCKSSQSLDSDGKTYLNW 60
QY 61 LLQKPGQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDTLTKISRVEAEDVGYYCWCQGTFFP 120

Db 61 LLQKPGQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDTLTKISRVEAEDVGYYCWCQGTFFP 120
QY 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132
Search completed: September 26, 2005, 07:16:20
Job time : 89 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 06:27:34 ; Search time 25 Seconds
(without alignments)
508.025 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTFFPRTFGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678	98.0	132	2 C32513	Ig kappa chain pre
2	587	84.8	131	2 S31577	Ig kappa chain - m
3	566	81.8	113	2 F30560	Ig kappa chain v r
4	554	80.1	112	2 A55491	proteolytic antibo
5	548	79.2	112	2 A36259	Ig kappa chain v r
6	547	79.0	111	2 S20709	Ig kappa chain v r
7	536	77.5	112	2 PL0273	Ig kappa chain v r
8	516	74.6	133	2 S42611	HUNVK protein prec
9	515	74.4	101	2 A33730	Ig kappa chain v r
10	515	74.4	133	2 S23230	Ig kappa chain pre
11	513	74.1	142	2 S22902	Ig kappa chain v r
12	512	74.0	133	2 S40324	Ig kappa chain v r
13	508	73.4	133	1 K2HURP	Ig kappa chain pre
14	502.5	72.6	140	2 S22658	Ig kappa chain pre
15	496	71.7	133	1 A24452	Ig kappa chain pre
16	491	71.0	132	2 S40322	Ig kappa chain - h
17	485	70.1	103	2 PH1055	Ig light chain v r
18	476	68.8	91	2 S42186	Ig kappa chain v r
19	473	68.4	120	2 S42268	Ig kappa chain v r
20	473	68.4	120	2 S42267	Ig kappa chain v r
21	470	67.9	131	2 S09259	Ig kappa chain pre
22	466	67.3	103	2 PH1056	Ig light chain v r
23	463	66.9	126	2 S40312	Ig kappa chain - h
24	463	66.9	131	2 D29380	Ig kappa chain pre
25	462.5	66.8	131	2 S40355	Ig kappa chain - h
26	462	66.8	132	2 S26882	Ig kappa chain v r
27	461.5	66.7	114	2 S49572	Ig kappa chain pre
28	460	66.5	118	2 S40374	Ig kappa chain - h
29	458.5	66.3	114	2 B49002	Ig kappa chain v r

ALIGNMENTS

RESULT 1

C32513
Ig kappa chain precursor V region (BXW14) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: C32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: C32513
A;Molecule type: DNA
A;Residues: 1-132 <KOF>
A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 678; DB 2; Length 132;
Best Local Similarity 97.7%; Pred. No. 1.6e-51;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW	60
Db	1	MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW	60
Qy	61	LLQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDTLTKISRIEADLGLYYCWQGTFFP	120
Db	61	LLQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDTLTKISRIEADLGLYYCWQGTFFP	120
Qy	121	RTFGGGTKLEIK	132
Db	121	RTFGGGTKLEIK	132

RESULT 2

S31577
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31577
R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, January 1993
A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antic
A;Reference number: S31577
A;Accession: S31577
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <REC>
A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin


```
RESULT 7
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: PL0273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0273
A;Molecule type: mRNA
A;Residues: 1-112 <SHL>
A;Cross-references: UNIPROT:Q8K0F8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
F;55-61/Region: complementarity-determining 2
F;62-93/Region: framework 3
F;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 2.3e-39;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTSLVITIGQPASISCKSSQSLYRNKGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIBAEADLGLYYCWQGTTHFP 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEADLGVYVCVQGTTHFP 112

RESULT 8
S42611
HUNK protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42611
R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regi
A;Reference number: S42610; MUID:92138794; PMID:1370957
A;Accession: S42611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <SPA>
A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;
Best Local Similarity 74.0%; Pred. No. 1.4e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNQYVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNW 60
Db 1 MRLPAQLGLLMLWVPGSGDVMTQSPSLPVTILGPASISCKSSQSLVFSFGNTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIBAEADLGLYYCWQGTTHFP 120
Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEADVGYYCYMGAHWP 120

Qy 121 RTFGGGTKLEI 131
Db 121 LTFGGGTKVEI 131
```

```
RESULT 9
A33730
Ig kappa chain V region (1.60) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: A33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
A;Accession: A33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <LAW>
A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110
A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 101;
Best Local Similarity 98.0%; Pred. No. 1.3e-37;
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIBAEADLGLYYCWQGTTHFP 120
Db 62 GVPDRFTGSGSGTDFTLKISRVEADLGVYVCVQGTTHFP 100

RESULT 10
S23230
Ig kappa chain precursor V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23230
R;Kennedy, M.A.
J. Exp. Med. 173, 1033-1036, 1991
A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and lig
A;Reference number: S23230; MUID:91178438; PMID:1840606
A;Accession: S23230
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KEN>
A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 133;
Best Local Similarity 74.2%; Pred. No. 1.7e-37;
Matches 98; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNQYVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNW 60
Db 1 MRLPAQLGLLMLWVPGSGDVMTQSPSLPVTILGPASISCKSSQSLVYSDGNTHLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIBAEADLGLYYCWQGTTHFP 120
Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEADVGYYCYMGAHWP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 YTFGGGTKLEIK 132
```

```
RESULT 11
S22902
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S22902
R:Chastagner, P.; These, J.; Zouali, M.
Gene 101, 305-306, 1991
A:Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region us
A:Reference number: S22902; MUID:91276289; PMID:1905262
A:Accession: S22902
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-142 <CHA>
A:Cross-references: EMBL:X56510
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-126/Domain: immunoglobulin homology <IMM>

Query Match      74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 2.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
Db 12 MRLPAQLLGLLMLWVPGSGDVMTQSPSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGLYVCWQGTFFP 120
Db 72 FQQRPGQSPRLIYKVSNRDVGVPDRFSGSGSGDTFTLKISRVEAEDVGVYCYMQGTHWP 131

QY 121 RTFGGTTKLEI 131
Db 132 FTFGQGTTRLEI 142

RESULT 12
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40324
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match      74.0%; Score 512; DB 2; Length 133;
Best Local Similarity 74.4%; Pred. No. 3.1e-37;
Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 4 PAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQ 63
Db 1 PAQLLGLLMLWVPGSGDVLTQSPSLPVTLGQPASISCRSDQSLVSDGKTYLNWYQQ 60

QY 64 RPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGLYVCWQGTFFPRTF 123
Db 61 RPQSPRLIYKVSNRDVGVPDRFTGSGSGDTFTLEISRVEAEDVGVYCYMQGTHWPCTF 120

QY 124 GGQTKLEIK 132
Db 121 GGQTKVEIK 129

RESULT 13
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X59135
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      72.6%; Score 502.5; DB 2; Length 140;
```

```
K2HURP
Ig kappa chain precursor V-II region (RPMI) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A:Cross-references: UNIPROT:P06310
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into lai
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-115/Domain: immunoglobulin homology <IMM>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

Query Match      73.4%; Score 508; DB 1; Length 133;
Best Local Similarity 73.5%; Pred. No. 6.9e-37;
Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
Db 1 MRLPAQLLGLLMLWVPGSGDVMTQSPSLPVTLGQPASISCRSSQSLVSDGNTYLNW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGLYVCWQGTFFP 120
Db 61 FQQRPGQSPRLIYKVSNRDVGVPDRFSGSGSGDTFTLKISRVEAEDVGVYCYMQGTHWS 120

QY 121 RTFGGTTKLEIK 132
Db 121 WTFGQGTKEIK 132

RESULT 14
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; EMBL:X59135
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      72.6%; Score 502.5; DB 2; Length 140;
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 06:29:58 ; Search time 28 Seconds
(without alignments)
351.917 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLMIRETNG.....CWQGTHTFRTFGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	93.8	131	4	US-09-647-468-163
2	646	93.4	131	4	US-09-647-468-164
3	606	87.6	142	4	US-09-840-459-102
4	606	87.6	142	4	US-09-497-625A-102
5	571	82.5	113	4	US-09-698-705-7
6	571	82.5	218	4	US-09-698-705-12
7	562	81.2	353	4	US-09-203-958A-4
8	560	80.9	112	4	US-09-809-739-11
9	560	80.9	112	4	US-09-840-459-9
10	560	80.9	112	4	US-09-497-625A-9
11	560	80.9	257	4	US-09-419-788-113
12	559	80.8	112	4	US-09-647-468-149
13	559	80.8	112	4	US-09-647-468-150
14	556	80.3	112	4	US-09-840-459-54
15	556	80.3	112	4	US-09-497-625A-54
16	548	79.2	112	2	US-08-678-194-6
17	548	79.2	112	3	US-08-890-011-6
18	548	79.2	112	3	US-09-262-724-6
19	548	79.2	535	3	US-08-983-035A-38
20	538	77.7	112	4	US-09-809-739-16
21	538	77.7	112	4	US-09-840-459-14
22	538	77.7	112	4	US-09-497-625A-14
23	537	77.6	132	1	US-08-477-877B-91
24	537	77.6	132	2	US-08-472-281A-91
25	537	77.6	132	2	US-08-477-989B-91
26	533	77.0	112	4	US-09-809-739-17
27	533	77.0	112	4	US-09-840-459-15

28	533	77.0	112	4	US-09-497-625A-15	Sequence 15, Appl
29	530	76.6	112	4	US-09-809-739-15	Sequence 15, Appl
30	530	76.6	112	4	US-09-840-459-13	Sequence 13, Appl
31	530	76.6	112	4	US-09-497-625A-13	Sequence 13, Appl
32	527	76.2	114	4	US-09-840-459-106	Sequence 106, App
33	527	76.2	114	4	US-09-497-625A-106	Sequence 106, App
34	525	75.9	112	4	US-09-809-739-18	Sequence 18, Appl
35	525	75.9	112	4	US-09-840-459-107	Sequence 107, App
36	520	75.1	112	4	US-09-809-739-14	Sequence 14, Appl
37	520	75.1	112	4	US-09-840-459-12	Sequence 12, Appl
38	520	75.1	112	4	US-09-497-625A-12	Sequence 12, Appl
39	518	74.9	132	1	US-08-477-877B-84	Sequence 84, Appl
40	518	74.9	132	2	US-08-472-281A-84	Sequence 84, Appl
41	518	74.9	132	2	US-08-477-989B-84	Sequence 84, Appl
42	515	74.4	100	4	US-09-840-459-22	Sequence 22, Appl
43	515	74.4	100	4	US-09-497-625A-22	Sequence 22, Appl
44	515	74.4	135	1	US-08-259-372A-12	Sequence 12, Appl
45	515	74.4	135	1	US-08-468-671-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-647-468-163
; Sequence 163, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163

Query Match	93.8%	Score	649;	DB	4;	Length	131;
Best Local Similarity	93.9%	Pred. No.	5.8e-55;				
Matches	123;	Conservative	4;	Mismatches	4;	Indels	0;
						Gaps	0;
Qy	2	MSPAQFLFLVLMIRETNGYVVMVTQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNLW	61				
Db	1	MSPAQFLFLVLMIRETNGYVVMVTQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNLW	60				
Qy	62	LQPGQSPKRLIYLKSLDGVDPDRFTGSGSGTDTLTKISRIEADLGLYICWQGTTHFPR	121				
Db	61	LQPGQSPKRLIYLKSLDGVDPDRFTGSGSGTDTLTKISRIEADLGLYICWQGTTHFPR	120				
Qy	122	TFGGQTKLEIK	132				
Db	121	TFGGQTKLEIK	131				

RESULT 2
US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436

```

; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NACHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match      93.4%; Score 646; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-54;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 MSPAQFLLLVLTRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
        |||||
Db      1 MSPAQFLLLVLTARDINGDVLTQTPLTSLVTIGQPASVCKSSQSLDSDGKTYLNWL 60

QY      62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRIEAEDLGLYYCWQGTFFPR 121
        |||||
Db      61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

QY      122 TFGGTTKLEIK 132
        |||||
Db      121 TFGGTTKLEIK 131

RESULT 3
US-09-840-459-102
; Sequence 102, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-102

Query Match      93.4%; Score 646; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-54;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 MSPAQFLLLVLTRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
        |||||
Db      1 MSPAQFLLLVLTARDINGDVLTQTPLTSLVTIGQPASVCKSSQSLDSDGKTYLNWL 60

QY      62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRIEAEDLGLYYCWQGTFFPR 121
        |||||
Db      61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

QY      122 TFGGTTKLEIK 132
        |||||
Db      121 TFGGTTKLEIK 131

RESULT 4
US-09-497-625A-102
; Sequence 102, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-102

Query Match      87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 8.4e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      10 LLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSP 69
        |||||
Db      7 LLVLWIRETIGDVVMTQTPLTSLVTVGHGPASISCKSSQSLDSDGKTFLNWLLQRPQSP 66

QY      70 KRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRIEAEDLGLYYCWQGTTHPRTFFGGTKL 129
        |||||
Db      67 KRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRVEAEDLGVYYCWQGTTHPRTFFGGTKL 126

QY      130 EIK 132
        |||
Db      127 EIK 129

RESULT 5
US-09-698-705-7
; Sequence 7, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
US-09-698-705-7
```

```

; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NACHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match      87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 8.4e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      10 LLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSP 69
        |||||
Db      7 LLVLWIRETIGDVVMTQTPLTSLVTVGHGPASISCKSSQSLDSDGKTFLNWLLQRPQSP 66

QY      70 KRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRIEAEDLGLYYCWQGTTHPRTFFGGTKL 129
        |||||
Db      67 KRLIYLVSKLDSGVPDRFTGSGGTDFTLKISRVEAEDLGVYYCWQGTTHPRTFFGGTKL 126

QY      130 EIK 132
        |||
Db      127 EIK 129

RESULT 5
US-09-698-705-7
; Sequence 7, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
US-09-698-705-7
```

```

; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-698-705-7

Query Match      82.5%; Score 571; DB 4; Length 113;
Best Local Similarity 97.3%; Pred. No. 1.5e-47;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSTLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 112

RESULT 6
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      82.5%; Score 571; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 3.2e-47;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSTLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 112

RESULT 7
US-09-203-958A-4
; Sequence 4, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELLER, Tibor
; APPLICANT: GOLDSTEIN, Joel

; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-059CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match      81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 4e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 177 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 236
Qy 82 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 132
Db 237 GVPDRFTGSGSGTDFTLKISRVEADLGLVYCWQGTFFPRTFGGGTKLEIK 287

RESULT 8
US-09-809-739-11
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match      80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
```

```

Db      2 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFNLWLLQRPQSPKRLIYLVSKLDS 61
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      62 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 112

RESULT 9
US-09-840-459-9
; Sequence 9, Application US/09840459
; Patent No. 6936550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-9

Query Match      80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db      22 VVMTQTPLTSLVTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
      138 VLMTQAPLTLTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 197
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      198 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 248

RESULT 10
US-09-497-625A-9
; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23

Query Match      80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db      22 VVMTQTPLTSLVTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
      2 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFNLWLLQRPQSPKRLIYLVSKLDS 61
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      62 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 112

RESULT 11
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILDBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-113

Query Match      80.9%; Score 560; DB 4; Length 257;
Best Local Similarity 94.6%; Pred. No. 4.3e-46;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      22 VVMTQTPLTSLVTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
      138 VLMTQAPLTLTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 197
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      198 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 248

RESULT 12
US-09-647-468-149
; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
```

```

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-9

Query Match      80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      22 VVMTQTPLTSLVTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
      2 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFNLWLLQRPQSPKRLIYLVSKLDS 61
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      62 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 112

RESULT 11
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILDBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-113

Query Match      80.9%; Score 560; DB 4; Length 257;
Best Local Similarity 94.6%; Pred. No. 4.3e-46;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      22 VVMTQTPLTSLVTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
      138 VLMTQAPLTLTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 197
      82 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 132
      198 GVPDRFTGSGGTDFTLKISRVEAEDLGLYYCWCQGTFFPRTFGGTTKLEIK 248

RESULT 12
US-09-647-468-149
; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
```


APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 149
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 22 VVMTQPTLTSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVLTQPTLTSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 112

RESULT 13
US-09-647-468-150
Sequence 150, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 150
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 22 VVMTQPTLTSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVLTQPTLTSVTIGQPASVCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 132

Db 62 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 112
RESULT 14
US-09-840-459-54
Sequence 54, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-54

Query Match 80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 4e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Qy 22 VVMTQPTLTSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IQLTQSPPLTSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVAEDLGLVYCWQGTTHFPRTFGGTTKLEIK 112

RESULT 15
US-09-497-625A-54
Sequence 54, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 54
LENGTH: 112

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-54

Query Match      80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 4e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 IQLTQSPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEADLGVYICWQGTTHFPRTFGGKLEIK 132
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 GVPDRFTGSGSGTDFTLKISRVEADLGVYICWQGTTHFPRTFGGKLEIK 112
```

Search completed: September 26, 2005, 07:19:02
Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 07:14:55 ; Search time 521 Seconds
(without alignments)
103.124 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLVIRETNG.....CWQGFHPTFGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	692	100.0	132	14	US-10-010-942B-2
2	692	100.0	132	15	US-10-388-389-2
3	692	100.0	132	16	US-10-703-713-2
4	692	100.0	132	16	US-10-704-070-2
5	692	100.0	132	17	US-10-232-030-2
6	650	93.9	135	9	US-09-881-823-10
7	649	93.8	131	15	US-10-462-062-163
8	646	93.4	131	15	US-10-462-062-164
9	644	93.1	239	17	US-10-476-265-19
10	641	92.6	133	18	US-10-810-881A-49
11	640	92.5	132	14	US-10-010-942B-5

12	640	92.5	132	15	US-10-388-389-5	Sequence 5, Appli
13	640	92.5	132	16	US-10-703-713-5	Sequence 5, Appli
14	640	92.5	132	16	US-10-704-070-5	Sequence 5, Appli
15	640	92.5	132	17	US-10-232-030-5	Sequence 5, Appli
16	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appl
17	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appl
18	630	91.0	132	15	US-10-388-389-11	Sequence 11, Appl
19	630	91.0	132	16	US-10-703-713-11	Sequence 11, Appl
20	630	91.0	132	16	US-10-704-070-11	Sequence 11, Appl
21	630	91.0	132	17	US-10-232-030-11	Sequence 11, Appl
22	618	89.3	145	16	US-10-830-899-52	Sequence 52, Appl
23	618	89.3	145	16	US-10-830-899-58	Sequence 58, Appl
24	618	89.3	145	16	US-10-830-899-61	Sequence 58, Appl
25	618	89.3	145	17	US-10-861-662-52	Sequence 52, Appl
26	618	89.3	145	17	US-10-861-662-58	Sequence 58, Appl
27	618	89.3	145	17	US-10-861-662-61	Sequence 61, Appl
28	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
29	606	87.6	142	16	US-10-766-773-102	Sequence 102, App
30	606	87.6	142	16	US-10-766-610-102	Sequence 102, App
31	606	87.6	142	16	US-10-733-563-102	Sequence 7, Appli
32	571	82.5	113	17	US-10-937-046-7	Sequence 12, Appl
33	571	82.5	218	17	US-10-937-046-12	Sequence 4, Appli
34	562	81.2	353	10	US-09-203-958A-4	Sequence 4, Appli
35	562	81.2	353	18	US-10-764-131-4	Sequence 1, Appli
36	560	80.9	112	9	US-09-835-087-1	Sequence 11, Appl
37	560	80.9	112	9	US-09-809-739-11	Sequence 9, Appli
38	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
39	560	80.9	112	16	US-10-766-773-9	Sequence 9, Appli
40	560	80.9	112	16	US-10-766-610-9	Sequence 9, Appli
41	560	80.9	112	16	US-10-733-563-9	Sequence 12, Appl
42	560	80.9	112	17	US-10-855-013-12	Sequence 86, Appl
43	560	80.9	122	15	US-10-272-899A-86	Sequence 88, Appl
44	560	80.9	130	15	US-10-272-899A-88	Sequence 149, App
45	559	80.8	112	15	US-10-462-062-149	

ALIGNMENTS

RESULT 1
US-10-010-942B-2
; Sequence 2, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurliq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2

Query Match 100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLVIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60
Db 1 MMSPAQFLFLVLVIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
QY 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

RESULT 2

US-10-388-389-2
; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

Query Match 100.0%; Score 692; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
QY 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

RESULT 3

US-10-703-713-2
; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
QY 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

RESULT 4

US-10-704-070-2
; Sequence 2, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLW 60
QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRIBAEADLGLYYCQGTFFP 120
QY 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

```

; ORGANISM: Murine
US-09-881-823-10

Query Match          93.9%; Score 650; DB 9; Length 135;
Best Local Similarity 93.2%; Pred. No. 5.6e-53;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLW 60
Db 1 MMSPAQFLFLVLWIRETNGVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLSW 60

Qy 61 LLORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTFFP 120
Db 61 LLORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTFFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 LTFGAGTKLELK 132

RESULT 7
US-10-462-062-163
; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462.062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163

Query Match          93.8%; Score 649; DB 15; Length 131;
Best Local Similarity 93.9%; Pred. No. 6.7e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLW 61
Db 1 MSPAQFLFLVLWIRETNGVVMVTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLW 60

Qy 62 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTFFP 121
Db 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGLYYCWQGTFFP 120

Qy 122 TFGGGTKLEIK 132
Db 121 TFGGGTKLEIK 131

RESULT 8
US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

```



```
QY 121 RTFGGKLEIK 132
Db 121 RTFGGKLEIK 132

RESULT 11
US-10-010-942B-5
; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5

Query Match 92.5%; Score 640; DB 14; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLGLYVCWQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLGLYVCWQGTFFP 120

QY 121 RTFGGKLEIK 132
Db 121 RTFGGKLEIK 132

RESULT 13
US-10-703-713-5
; Sequence 5, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-703-713-5

Query Match 92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMVTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

QY 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLGLYVCWQGTFFP 120
Db 61 LLQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLGLYVCWQGTFFP 120

QY 121 RTFGGKLEIK 132
Db 121 RTFGGKLEIK 132

RESULT 14
US-10-704-070-5
; Sequence 5, Application US/10704070
```

```
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-704-070-5

Query Match          92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
    |||||
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
    |||||

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDGLYYCWOQTHFP 120
    |||||
Db 61 LLQKPQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGYYVCWOQTHFP 120
    |||||

Qy 121 RTFGGGTKLEIK 132
    |||||
Db 121 RTFGGGTKVEIK 132
    |||||

RESULT 15
US-10-232-030-5
; Sequence 5, Application US/10232030
; Publication No. US2005009150A1
; GENERAL INFORMATION:
; APPLICANT: Dale Schenk
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CN
; CURRENT APPLICATION NUMBER: US/10/232,030
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 09/723,713
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-232-030-5

Query Match          92.5%; Score 640; DB 17; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.7e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
    |||||
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
    |||||

Qy 61 LLQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDGLYYCWOQTHFP 120
    |||||
Db 61 LLQKPQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGYYVCWOQTHFP 120
    |||||

Qy 121 RTFGGGTKLEIK 132
    |||||
Db 121 RTFGGGTKVEIK 132
    |||||

Search completed: September 26, 2005, 07:27:49
Job time : 521 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 04:38:08 ; Search time 2359 Seconds
(without alignments)
6389.763 Million cell updates/sec

Title: US-10-010-942B-1
Perfect score: 396
Sequence: 1 atgatgagctctgccagtt.....gcaccaagctggaatacaaa 396

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gse1:*
- 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368.8	93.1	773	4	BG964451 602832101
2	357.6	90.3	909	4	BI105366 602893669
3	312.4	78.9	926	2	BF301241 602029676
4	311.2	78.6	783	6	CB316492 AGENCOURT
5	310.8	78.5	407	5	BY223114 BY223114
6	307.8	77.7	357	5	BY344116 BY344116
7	306	77.3	618	8	AZ938720 2M0197H20
8	300.4	75.9	356	5	BY216837 BY216837
9	297.8	75.2	883	2	BF134462 601784859
10	290.4	73.3	346	5	BY216432 BY216432
11	290.4	73.3	346	5	BY219888 BY219888
12	288.2	72.8	355	5	BY217354 BY217354
13	274.4	69.3	342	5	BY215445 BY215445
14	266	67.2	312	5	BY346516 BY346516
15	263.2	66.5	960	5	BQ711007 AGENCOURT
16	260.8	65.9	833	7	CO565696 AGENCOURT
17	260.6	65.8	898	5	BQ708918 AGENCOURT
18	260	65.7	525	6	CD696039 EST12562
19	258.4	65.3	634	4	BM783161 K-EST0061
20	257.6	65.1	952	4	BG758592 602712820
21	256.8	64.8	681	5	BU930837 AGENCOURT
22	256.8	64.8	816	4	BI759427 603043095
23	255.8	64.6	614	2	AW405187 UI-HF-BLO
24	255.2	64.4	475	6	CD699289 EST15812

25	255.2	64.4	638	6	CD695306	CD695306 EST11829
26	255.2	64.4	683	6	CD702671	CD702671 EST19196
27	254.2	64.2	767	6	CB985229	CB985229 AGENCOURT
28	253.6	64.0	498	6	CD699812	CD699812 EST16336
29	253.6	64.0	562	6	CD690641	CD690641 EST7164 h
30	253.6	64.0	600	6	CD700169	CD700169 EST16693
31	253.6	64.0	755	6	CB985900	CB985900 AGENCOURT
32	252.2	63.7	541	6	CD707996	CD707996 EST24523
33	252	63.6	524	6	CD700306	CD700306 EST16830
34	252	63.6	597	6	CD689298	CD689298 EST5820 h
35	252	63.6	701	4	BG547597	BG547597 602575437
36	252	63.6	743	6	CB987308	CB987308 AGENCOURT
37	252	63.6	815	6	CB985592	CB985592 AGENCOURT
38	250.4	63.2	513	6	CD692011	CD692011 EST8534 h
39	250.4	63.2	599	6	CD687299	CD687299 EST3820 h
40	250.4	63.2	700	6	CB987545	CB987545 AGENCOURT
41	250.4	63.2	745	6	CB987813	CB987813 AGENCOURT
42	250.4	63.2	763	6	CB985041	CB985041 AGENCOURT
43	250.4	63.2	773	6	CB959401	CB959401 AGENCOURT
44	250.4	63.2	774	4	BM007808	BM007808 603617276
45	250.4	63.2	817	6	CB957285	CB957285 AGENCOURT

ALIGNMENTS

RESULT 1
BG964451
LOCUS 602832101F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4986529 5',
DEFINITION 773 bp mRNA linear EST 12-JUN-2001
ACCESSION BG964451
VERSION BG964451.1 GI:14352088
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10996 row: b column: 02
High quality sequence stop: 732.
Location/Qualifiers
1. 773
/organism="Mus musculus"
/mol type="mRNA"
/strain="FVB/N"
/db xref="IMAGE:4986529"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES
source

ORIGIN

Query Match 93.1%; Score 368.8; DB 4; Length 773;
Best Local Similarity 95.7%; Pred. No. 1.9e-105;
Matches 379; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTCTCTGATTCGGGAACCAACCGT 60

Query Match	78.9%;	Score 312.4;	DB 2;	Length 926;
Best Local Similarity	96.7%;	Pred. No. 1.6e-87;		
Matches 383;	Conservative	0;	Mismatches 6;	Indels 7; Gaps 6;

Qy	1	ATGATGAGTCTGCCCCAGTTTCCTGTTTAGTGCTCTGGATTTCGGGAACCAACCGGT	60
Db	43	ATGATGAGTCTGCCCCAGTTTCCTGTTTAGTGCTCTGGATTTCGGGAACCAACCGGT	102
Qy	61	TATGTTGTGATGACCCAGACTCCCACTCACTTTGTTCGGTTACCATTGGACAACCGCCTCC	120
Db	103	GATG-TGTGATGACCCAGACTCCCACTCAC-TTGTTCGGTTACCA-TGGACAACCGCCTCC	159
Qy	121	ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTATAGTATGGAAGACATATTGAAATGG	180
Db	160	ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTATGGAAGACATATTGAAAT--G	217
Qy	181	TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTTGTTTAAACTGGAC	240
Db	218	GTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAAATCTATCTGTTGTTTAAACTGGAC	277
Qy	241	TCTGGAGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	300
Db	278	TCTGGAGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC	337
Qy	301	AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT	360
Db	338	AGCAGAGTGGAGGCTGAGGA-TTGGGAGTTTATTATTGCTGGCAAGGTACATTTTCCT	396
Qy	361	CGGACGTTTCGTTGGAGGCACCAAGCTTGGAAATCAA	396
Db	397	-GGACGTTTCGTTGGAGGCACCAAGCTTGGAAATCAA	431

RESULT 4

CB316492

LOCUS

AGENCOURT 11790259 NICHDRr Pit1 Rattus norvegicus cDNA clone

IMAGE:6890409 5', mRNA sequence.

CB316492

CB316492.1 GI:28840727

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .783

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="IMAGE:6890409"

/tissue_type="Pituitary"

/lab_host="DH10B"

/clone_lib="NICHDRr Pit1"

/note="Vector: pDNRR-LiB; Site 1: Sfil; Site 2: Sfil; 5'

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..407

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NOD"

/db_xref="taxon:10090"

/clone="F830301N12"

/tissue_type="activated spleen"

/clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN

Query Match 78.5%; Score 310.8; DB 5; Length 407;

Best Local Similarity 92.1%; Pred. No. 4.1e-87;

Matches 350; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTTCGGGAACCAACGGT 60

|||||

Db 31 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTCGATTTCAGGAACCAACGGT 90

|||||

QY 61 TATGTTGTGATGACCCAGATCCCACTCACTTTGTCGGTTACCAATGGACACCAAGCCTCC 120

|||||

Db 91 GATGTTGTGATGACTCAGACCCCACTCACTTTGTCGGTTACCAATGGACACCAAGCCTCC 150

QY 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGGAAGACATATTTGAATTGG 180

|||||

Db 151 ATCTCTTGCAATCAAGTCAGAGCCTCTTACATAGTAATGGAAGACATATTTGAATTGG 210

|||||

QY 181 TTGTTACAGAGGCCAGGCCAGTCTTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC 240

|||||

Db 211 TTATTACAGAGGCCAGGCCAGTCTTCCAAAGCTCCTAATCTATCTGGTGTCTAAACTGGAA 270

|||||

QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGCATCAGGACAGATTTTACACTGAAATC 300

|||||

Db 271 TCTGGAGTCC--TGACAGGTCAGTGGCAGTGCATCAGGACAGATTTTACACTGAAATC 328

|||||

QY 301 AGCAGATAGAGGCTGAGGATTTGSGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360

|||||

Db 329 AGCAGAGTGGAGGCTGAGGATTTGGGA-GTTATTACTGCTTGGCAAGCTACACATTTTCCT 387

|||||

QY 361 CGGACGTTCCGTTGGAGGCAC 380

|||||

Db 388 CAGACGTTCCGTTGGAGGCAC 407

RESULT 6

BY344116

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY344116 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L730002K22 5', mRNA sequence.

BY344116

BY344116.1 GI:26573604

EST.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 357)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece) whose assistance we gratefully
acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES source
Location/Qualifiers
1. .357
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L730002K22"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"

ORIGIN
Query Match 77.7%; Score 307.8; DB 5; Length 357;
Best Local Similarity 96.3%; Pred. No. 3.5e-86;
Matches 315; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTCGCCAGTCCCTGTTCTGTTAGTGTCTGATTCGGAAACCAACGGT 60
Db 31 ATGATGAGTCTCGCCAGTCCCTGTTCTGTTAGTGTCTGATTCGGAAACCAACGGT 90
QY 61 TATGTTGTGATGACCCAGTCCACTCCTTGTGCTGTTACCATTTGGAAACCAACCTCC 120
Db 91 GATGTTGTGATGACCCAGTCCACTCCTTGTGCTGTTACCATTTGGAAACCAACCTCT 150
QY 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATATTTGATTGG 180
Db 151 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATATTTGATTGG 210
QY 181 TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTCTAAACCTGGAC 240
Db 211 TTATTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTCTAAACCTGGAC 270
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAGACAGATTTTACACTGAAATC 300
Db 271 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAGACAGATTTTACACTGAAATC 330
QY 301 AGCAGAATAGAGGCTGAGGATTTGGGA 327
Db 331 AGCAGAGTGGAGGCTGAGGATTTGGGA 357

RESULT 7
AZ938720 618 bp DNA linear GSS 26-APR-2001
LOCUS AZ938720 Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION 2M0197H20F

clone UUGC2M0197H20 F, genomic survey sequence.
AZ938720
AZ938720.1 GI:13798758
GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 618)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0197 row: H column: 20
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 618.

FEATURES source
Location/Qualifiers
1. .618
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0197H20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 77.3%; Score 306; DB 8; Length 618;
Best Local Similarity 96.6%; Pred. No. 1.5e-85;
Matches 312; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 43 ATTCGGGAAACCAACGGTATGTTGTGATGACCCAGACTCCACTCCTTGTGCGTTACC 102
Db 228 ATTTCAAGAACCAACGGTATGTTGTGATGACCCAGACTCCACTCCTTGTGCGTTACC 287
QY 103 ATTGGACAAACAGCCTCCATCTTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGGA 162
Db 288 ATTGGACAAACAGCCTCCATCTCTTGGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGGA 347
QY 163 AAGACATATTGAATTGGTTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTAT 222

||||| 348 AAGACATATTTGAATTTGGTTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCTAATCTAT 407
QY 223 CTGGTGCTAAACTGGACTCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGAGCA 282
Db 408 CTGGTGCTAAACTGGACTCTGGAGTCCCTGACAGGTTTCACTGGCAGTGGATCAGGAGCA 467
QY 283 GATTTTACACTGAAAATCAGCAGAAATAGAGGCTGAGGATTTGGACTTTTATTATTGCTGG 342
Db 468 GATTTTCACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGAGTNTATTATTGCTGG 527
QY 343 CAAGGTACACATTTTCTCTCGGAC 365
Db 528 CAAGGTACACATTTTCTCTCACAC 550

RESULT 8
BY216837
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BY216837 356 bp mRNA linear EST 10-DEC-2002
CDNA clone F830047E03 5', mRNA sequence.
BY216837
BY216837.1 GI:26397609
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Guatinchich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempole, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source
1..356
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830047E03"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN

Query Match 75.9%; Score 300.4; DB 5; Length 356;
Best Local Similarity 95.1%; Pred. No. 7.8e-84; Indels 0; Gaps 0;
Matches 310; Conservative 0; Mismatches 16;
QY 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTCTGTGGATTCGGGAACCAACGGT 60
Db 31 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTCTGTGGATTCGGGAACCAACGGT 90
QY 61 TATGTTCTGATGACCCAGACTCCACTCATTGTCGGTTACCAATGGACACACGCTCC 120
Db 91 GATGTTGATGATGACTCAGACCCCACTTGTTCGGTTACCAATGGACACACGCTCC 150
QY 121 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTAGATAGTATGATGGAACACATATTGAATTGG 180
Db 151 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTAGATAGTATGATGGAACACATATTGAATTGG 210
QY 181 TTGTTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTAAACTGGAC 240
Db 211 TTATTACAGAGGCCAGGCCAGTCTCCAAAGCTCCTAATCTATCTGTTGTTAAACTGGAA 270
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300
Db 271 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 330
QY 301 AGCAGATAGAGGCTGAGGATTTGGG 326
Db 331 AGCAGATAGAGGCTGAGGATTTGGG 356

RESULT 9
BF134462
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
BF134462 883 bp mRNA linear EST 24-OCT-2000
601784859P1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012790 5',
mRNA sequence.
BF134462 GI:10973502
Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 883)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9254 row: e column: 15
High quality sequence stop: 708.
Location/Qualifiers
1. 883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4012790"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

FEATURES
source
Query Match 75.2%; Score 297.8; DB 2; Length 883;
Best Local Similarity 94.2%; Pred. No. 6.7e-83;
Matches 374; Conservative 0; Mismatches 17; Indels 6; Gaps 6;
QY 1 ATGATGAGTCCTGCCCGCTTCCTGTTCTGTTAGTCTCTGGATTCGGAAACCAACGGT 60
Db 19 ATGATGAGTCCTGCCCGCTTCCTGTTCTGTTAGTCTCTGGATTCAGGAACCAACGGT 78
QY 61 TATGTTGTGATGACCCAGACTCCACTCCTTGTGCTGTTACCATTTGGACAACCAACGCTCC 120
Db 79 GATG-TGTGATGACTCAGACCCCACTCAC-TTGTGCGTTACCA-TGGACAACCAACGCTCC 135
QY 121 ATCTCTT-GCAAGTCAAGTCAGACCTCTTAGATAGTATGATGGAAGACATATTTGAATTG 179
Db 136 ATCTCTTGGCAAGTCAAGTCAGAGCTCTTACATAGTAATGGAAGACATATTTGAA-TG 194
QY 180 GTTGTGTACAGAGCCAGGCCAGTCCTCCAAAGCGCCTTAATCTATCTGTGTCTAACTGGA 239
Db 195 GTTATACAGAGGCCAGGCCAGTCCTCCAAAGCTCCTAATCTATCTGTGTCTAACTGGA 254
QY 240 CTCTGAGTCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAT 299
Db 255 ATCTGAGTCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAT 314
QY 300 CAGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTATTCGTGCGCAAGGTACACATTTTCC 359
Db 315 CAGCAGAGTGGAGGCTGAGGA-TTGGGAGTTTATTACTGCTTGTCAAGCTACACATTTTCC 373
QY 360 TCGGAGCTTCGTGGAGGACCAAGCTGGAATCAAA 396
Db 374 TCGGAGCTTCGTGGAGGACCAAGCTGGAATCAAA 410

RESULT 10
BY216432 346 bp mRNA linear EST 10-DEC-2002
LOCUS
DEFINITION
BY216432 RIKEN full-length enriched, activated spleen Mus musculus
CDNA clone F830044L02 5', mRNA sequence.

ACCESSION BY216432
VERSION GI:26397182
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 346)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuoka, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES	
source	Location/Qualifiers
	1..346
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="NOD"
	/db_xref="taxon:10090"
	/clone="F83004L02"
	/tissue type="activated spleen"
	/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN	
Query Match	73.3%; Score 290.4; DB 5; Length 346;
Best Local Similarity	94.9%; Pred. No. 1.1e-80;
Matches 300; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
Qy	1 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTGTCTGTGATTCGGGAACCAACCGT 60
Db	
Qy	31 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTGTCTGTGATTCAGGAACCAACCGT 90
Db	
Qy	61 TATGTTGTGATGATCCAGACTCCACTCTCTGTCGTTTACCTGGACACCAAGCTCC 120
Db	
Qy	91 GATGTTGTGATGATCTAGACCCCACTACTTTGTGGTTACCATGGACACCAAGCTCC 150
Db	
Qy	121 ATCTCTTCAAGTCAAGTCAGACCTCTTAGATAGTGTGGAAGACATATTGAATTGG 180
Db	
Qy	151 ATCTCTTCAAGTCAAGTCAGACCTCTTACATAGTAATGGAAGACATATTGAATTGG 210
Db	
Qy	181 TTGTTACAGAGCGCCAGTCTCCAAAGCGCTTAATCTATCTGTGTCTPAAACTGGAC 240
Db	
Qy	211 TTATTACAGAGCGCCAGTCTCCAAAGCTCTTAATCTATCTGTGTCTPAAACTGGAA 270
Db	
Qy	241 TCTGGAGTCCCTGACAGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300
Db	
Qy	271 TCTGGAGTCCCTGACAGTTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 330
Db	
Qy	301 AGCAGATPAGAGGCTG 316
Db	
Qy	331 AGCAGATPAGAGGCTG 346
Db	

RESULT 11
BY219888
LOCUS
DEFINITION
CDNA clone F830117N11 5', mRNA sequence.
BY219888
BY219888.1 GI:26400953
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 346)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, I., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempole, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES	
Location/Qualifiers	source
1..346	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="NOD"
	/db_xref="taxon:10090"
	/clone="F830117N11"
	/tissue type="activated spleen"
	/clone_lib="RIKEN full-length enriched, activated spleen"
ORIGIN	
Query Match	73.3%; Score 290.4; DB 5; Length 346;
Best Local Similarity	94.9%; Pred. No. 1.1e-80;
Matches 300; Conservative	0; Mismatches 16; Indels 0; Gaps 0;

Qy	1 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTGTCTGTGATTCGGGAACCAACCGT 60
Db	
Qy	31 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTGTCTGTGATTCAGGAACCAACCGT 90
Db	
Qy	61 TATGTTGTGATGATCCAGACTCCACTCTTGTTCGGTTACCATTTGGACAACCAAGCTCC 120
Db	
Qy	91 GATGTTGTGATGATCAGACCCCACTCACTTTGTCGGTTACCATTTGGACAACCAAGCTCC 150
Db	

QY 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAGGACATATTTGAATTGG 180
 |||
 Db 151 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAGGACATATTTGAATTGG 210
 |||
 QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGTGTCTAAACTGGAC 240
 |||
 Db 211 TTATTACAGAGCCAGCCAGTCTCCAAAGCTCCTAATCTATCTGTGTCTAAACTGGAA 270
 |||
 QY 241 TCTGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
 |||
 Db 271 TCTGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 330
 |||
 QY 301 AGCAGAAATAGAGGCTG 316
 |||
 Db 331 AGCAGAGTGGAGGCTG 346
 |||

RESULT 12

BY217354 355 bp mRNA linear EST 10-DEC-2002
 LOCUS BY217354 RIKEN full-length enriched, activated spleen Mus musculus
 DEFINITION CDNA clone F830050M02 5', mRNA sequence.

ACCESSION BY217354

VERSION BY217354.1 GI:26398178

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawayawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 1246851

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Source

Location/Qualifiers

1..355

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NOD"

/db_xref="taxon:10090"

/clone="F830050M02"

/tissue_type="activated spleen"

/clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN

Query Match 72.8%; Score 288.2; DB 5; Length 355;
 Best Local Similarity 92.9%; Pred. No. 5.8e-80;
 Matches 302; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 ATGATGAGTCTGCCAGTTCCTGTTCTGTAGTCTCTGGATTCGGAAACCAACGGT 60

|||||

Db 31 ATGATGAGTCTGTCAGTTCCTGTTCTGTATGCTCTGGATTCAGGAACCAATGGT 90

|||||

QY 61 TATGTTGATGACCCAGACTCCACTCTTGTGCTTACCATTTGGACCAACCCCTCC 120

|||||

Db 91 GATGTTGATGACCCAGACTCCACTGCTTTGTCGTTACCATTTGGACCAACCCCTCT 150

|||||

QY 121 ATCTCTTGCAGTCAAGTCAGACCTCTTAGATAGTGAAGGACATATTTGAATTGG 180

|||||

Db 151 ATCTCTTGCAGTCAAGTCAGACCTCTTAGATAGTGAAGGACATATTTGAATTGG 210

|||||

QY 181 TTGTTACAGAGCCAGCCAGTCTCCAAAGCGCTTAATCTATCTGGTGTCTAACTGGAC 240

|||||

Db 211 TTACAACAGAGCCAGCCAGTCTCCAAAGCGCTTAATGTATCAGGTGTCCAACTGGAC 270

|||||

QY 241 TCTGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300

|||||

Db 271 CCTGGCATCCCTGACAGGTTCACTGGCAGTGGATCAGAGACAGATTTTACACTTAAATC 330

|||||

QY 301 AGCAGAAATAGAGGCTGAGGATTGG 325

|||||

Db 331 AGCAGAGTGGAGGCTGAGGATTGG 355

RESULT 13

BY215445

LOCUS

DEFINITION BY215445 RIKEN full-length enriched, activated spleen Mus musculus

CDNA clone F830037C03 5', mRNA sequence.

ACCESSION BY215445

VERSION BY215445.1 GI:26396173

BY215445 342 bp mRNA linear EST 10-DEC-2002

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 342)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K.,
Sultan,A., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,L., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for

FEATURES
source
Location/Qualifiers
1. .342
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830037C03"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN
Query Match 69.3%; Score 274.4; DB 5; Length 342;
Best Local Similarity 94.6%; Pred. No. 1.4e-75;
Matches 295; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
Qy 1 ATGATGAGTCCTGCCAGTTCCTGTTCTGTTAGTCTGTTGGATTCCGGAAACCAACGGT 60
Db 31 ATGATGAGTCCTGCCAGTTCCTGTTCTGTTAGTCTGTTGGATTCCGGAAACCAACGGT 90
Qy 61 TATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACACCAACGCTCC 120
Db 91 GATGTTGTGATGACTCAGACCCCACTCATTGTCGGTTACCATTTGGACACCAACGCTCC 150
Qy 121 ATCTCTTGAAGTCAAGTCAGAG-CCTCTTAGATAGTATGATGGAAGACATATTTGAATTG 179
Db 151 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTACATAGTAATGGAAGACATATTTGAATTG 210
Qy 180 GTTGTGTACAGAGCCAGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGA 239
Db 211 GTTATTACAGAGCCAGCCAGTCTCCAAAGCTCCTAATCTATCTGGTGTCTAAACTGGA 270
Qy 240 CTCTGGAGTCCTTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAT 299
Db 271 ATCTGGAGTCCTTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAT 330
Qy 300 CAGCAGAATAGA 311
Db 331 CAGCAGAGTGA 342

RESULT 14
BY346516
LOCUS
DEFINITION
BY346516 RIKEN full-length enriched, whole joints Mus musculus cDNA
clone L730024N10 5', mRNA sequence.
ACCESSION
BY346516.1 GI:26576004
VERSION
BY346516.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 312)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K.,
Sultan,A., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9225

	Query Match	67.2%	Score 266;	DB 5;	Length 312;
	Best Local Similarity	96.5%	Pred. No. 6.1e-73;		
	Matches 272;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	1	ATGATGAGTCCTGCCCACTTCCTGTTTCTGTTAGTGCCTCTGGATT	CGGAAACCAACGGT	60	
	31	ATGATGAGTCCTGACCACTTCCTGTTTCTGTTAGTGCCTCTGGATT	CAGGAAACCAACGGT	90	
Qy	61	TATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGTTACCAATTGGA	CAACCGCCTCC	120	
Dd	91	GATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGTTACCAATTGGA	CAACCGCCTCT	150	
Qy	121	ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTATGGAAGACATATTGA	ATTGG	180	

Db	151	ATCTCTTGGCAAGTCAAGTCAGAGCCCTCTTATATAGTAATGGAAAAACCTATTATTGGAATTGG	210
Qy	181	TTGTTTACAGAGCGGCAGGCCAGTCTCCAAAGCGCCCTAATCTATCTGGTGTCTAAACTGGAC	240
Db	211	TTATTACAGAGCGGCAGGCCAGTCTCCAAAGCGCCCTAATCTATCTGGTGTCTAAACTGGAC	270
Qy	241	CTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACA	282
Db	271	CTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAACA	312

RESULT 15
BQ7111007
LOCUS BQ7111007 .960 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7975525 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215018
5', mRNA sequence.

```
Db      183  TACCTGCAGAAAGCCAGGCCAGCCTCCACAGCTCCTGATCTATGAGGTTTCCAAACCGGTTT 242
Qy      241  TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
Db      243  TCTGGAGTCCAGATAGGTTTCAGTGGCAGCGGTCAGGGACAGATTTTCACACTGAAAATC 302
Qy      301  AGCAGAAATAGAGGCTGAGGATTTGGGACTTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
Db      303  AGCCGGGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAAAGTATACAGTTTCCT 362
Qy      361  CGGACGTTCCGTGGAGGCCACCAAGCTGGAATCAAA 396
Db      363  CTCACCTTCGGCGGAGGGACCAAGGTGGAGATCAAA 398
```

Search completed: September 26, 2005, 06:27:24
Job time : 2364 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 01:45:09 ; Search time 393 Seconds
(without alignments)
5964.930 Million cell updates/sec

Title: US-10-010-942B-1
Perfect score: 396
Sequence: 1 atgatgagtcctgccagtt.....gcaccaagctggaatcaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		N_Geneseq_16Dec04:*	
1:	Geneseqn1980s:*	1	396
2:	Geneseqn1990s:*	2	384
3:	Geneseqn2000s:*	3	370.6
4:	Geneseqn2001as:*	4	368.8
5:	Geneseqn2001bs:*	5	365.8
6:	Geneseqn2002as:*	6	364
7:	Geneseqn2002bs:*	7	361
8:	Geneseqn2003as:*	8	360.8
9:	Geneseqn2003bs:*	9	361
10:	Geneseqn2003cs:*	10	360.8
11:	Geneseqn2003ds:*	11	360.8
12:	Geneseqn2004as:*	12	359.8
13:	Geneseqn2004bs:*	13	344.8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	396	100.0	396	13	ADR88405
2	384	97.0	384	6	ABS59426
3	370.6	93.6	717	12	ADP45590
4	368.8	93.1	420	6	ABN84610
5	365.8	92.4	717	12	ADM72032
6	364	91.9	717	8	ABZ24632
7	364	91.9	1953	8	ABZ24634
8	361	91.2	393	2	AAZ33016
9	361	91.2	393	2	AAZ33017
10	360.8	91.1	426	2	AAQ12063
11	360.8	91.1	426	2	AAQ12019
12	359.8	90.9	729	8	ABX16570
13	344.8	87.1	737	2	AAQ25691
14	335.4	84.7	426	4	AAQ13177
15	335.4	84.7	426	13	ADQ89317
16	335.4	84.7	426	13	ADQ89323
17	324.2	81.9	717	12	ADM72034
18	322.2	81.4	1135	2	AAQ58936
19	317.2	80.1	976	2	AAQ25665
20	315.8	79.7	336	9	ACC84730

21	315.8	79.7	336	12	ADQ31244	Adq31244 Murine 1A
22	315.2	79.6	486	10	ADQ6759	Adq6759 D13 light
23	312.8	79.0	336	2	AAV20601	Aav20601 A77 anti-
24	312.8	79.0	336	4	AAF74891	Aaf74891 A77 anti-
25	312.8	79.0	336	4	AAJ15262	Aaj15262 Murine A7
26	312.6	78.9	729	2	AAV36236	Aav36236 DNA of Sc
27	310	78.3	366	12	ADJ95989	Adj95989 Immunoglo
28	310	78.3	390	12	ADJ95991	Adj95991 Immunoglo
29	309.8	78.2	1749	13	ADSI7377	Adsi7377 Nucleotid
30	309.6	78.2	381	4	AAH21232	Aah21232 Murine de
31	307.8	77.7	768	2	AAT48000	Aat48000 Coding se
32	306.6	77.4	315	2	AAQ20307	Aaq20307 B cell hy
33	306.2	77.3	336	9	ACF79290	Acf79290 Monoclona
34	306.2	77.3	339	10	ADD05269	Add05269 Female mo
35	306.2	77.3	339	12	ADM80360	Adm80360 Murine ho
36	306.2	77.3	749	2	AAT86234	Aat86234 Anti-huma
37	306.2	77.3	1611	2	AAT86221	Aat86221 Human p53
38	303.2	76.6	342	12	ADI26468	Adi26468 Murine I4
39	301.4	76.1	336	10	ADE13217	Ade13217 Humanised
40	301.4	76.1	339	3	ABK15814	Abk15814 DNA encod
41	301.4	76.1	339	3	AAA62120	Aaa62120 Mouse HBV
42	301	76.0	685	4	AAH77316	Aah77316 IgG Fab-B
43	298.2	75.3	819	2	AAT86646	Aat86646 Mus muscu
44	296.6	74.9	336	2	AAQ58687	Aaq58687 Monoclona
45	296.6	74.9	336	5	AAI70097	Aai70097 Type II c

ALIGNMENTS

RESULT 1	
ADR88405	
ID	ADR88405 standard; DNA; 396 BP.
XX	
AC	ADR88405;
XX	
DT	16-DEC-2004 (first entry)
XX	
DE	Murine 3D6 immunoglobulin light chain variable region DNA SEQ ID NO:1.
XX	
KW	ds; 3D6; light chain variable region; immunoglobulin;
KW	complementarity determining region; CDR; 10D5; variable framework region;
KW	neuroprotective; nontropic; gene therapy; amyloidogenic disease;
KW	Alzheimer's disease.
XX	
OS	Mus musculus.
XX	
PH	Key
CDS	Location/Qualifiers
FT	1..396
FT	/*tag= b
FT	/partial
FT	/note= "no stop codon given"
FT	/product= "3D6 immunoglobulin light chain variable
FT	region"
FT	1..60
FT	/*tag= a
FT	mat_peptide
FT	61..393
FT	/*tag= c
XX	
PN	WO2004080419-A2.
XX	
PD	23-SEP-2004.
XX	
PF	12-MAR-2004; 2004WO-US0007503.
XX	
PR	12-MAR-2003; 2003US-00388389.
XX	
PA	(NEUR-) NEURALAB LTD.
PA	(AMHP) WYETH.
XX	
PI	Basi G, Saldanha JW, Yednock T;
XX	
DR	WPI; 2004-668880/65.

DR N-PSDB; ADR88406.
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX
XX Claim 76; SEQ ID NO 1; 176pp; English.
PS
CC The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence encodes the murine 3D6
CC immunoglobulin light chain variable region.
XX
SQ Sequence 396 BP; 101 A; 88 C; 99 G; 108 T; 0 U; 0 Other;

Query Match 100.0%; Score 396; DB 13; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.2e-119;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGCGGAAACCAACGGT 60
Db 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGCGGAAACCAACGGT 60
QY 61 TATGTTGTGATGACCCAGACTCCACTCTTGTTCGGTTACCATTTGGACACCGCTCC 120
Db 61 TATGTTGTGATGACCCAGACTCCACTCTTGTTCGGTTACCATTTGGACACCGCTCC 120
QY 121 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
Db 121 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
QY 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTCTTAAACTGGAC 240
Db 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTCTTAAACTGGAC 240
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
Db 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
QY 301 AGCAGAAATAGAGGCTGAGGATTTGGGACTTTTATTGTTGCGGCAAGGTACACATTTTCCT 360
Db 301 AGCAGAAATAGAGGCTGAGGATTTGGGACTTTTATTGTTGCGGCAAGGTACACATTTTCCT 360
QY 361 CGGACGTTTCGGTGGAGGCCACCAAGCTGGAATCAA 396
Db 361 CGGACGTTTCGGTGGAGGCCACCAAGCTGGAATCAA 396

RESULT 2
AB559426
ID AB559426 standard; DNA; 384 BP.
XX
AC
XX AB559426;

DT 05-NOV-2002 (first entry)
XX Mouse 3D6 VL gene.
DE
XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW neurotropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta; gene; ds.
XX
OS Mus musculus.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
PI Basi G, Saldanha J, Yednock T;
XX
XX WPI; 2002-519658/55.
DR P-PSDB; ABG76923.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 76; Page 79; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present nucleic
CC acid sequence encodes a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 384 BP; 95 A; 86 C; 97 G; 106 T; 0 U; 0 Other;
Query Match 97.0%; Score 384; DB 6; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGCGGAAACCAACGGT 60
Db 1 ATGATGAGTCTCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGCGGAAACCAACGGT 60
QY 61 TATGTTGTGATGACCCAGACTCCACTCTTGTTCGGTTACCATTTGGACACCGCTCC 120
Db 61 TATGTTGTGATGACCCAGACTCCACTCTTGTTCGGTTACCATTTGGACACCGCTCC 120
QY 121 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
Db 121 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 180
QY 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTCTTAAACTGGAC 240
Db 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCTTAATCTATCTGTTCTTAAACTGGAC 240
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
Db 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAATC 300
QY 301 ACAGAAATAGAGGCTGAGGATTTGGGACTTTTATTGTTGCGGCAAGGTACACATTTTCCT 360

|||||
301 AGCAGATAGAGGCTGAGGATTTGGGACTTTATTAATGCTGGCAAGGTACACATTTTCCT 360
361 CGGACGTTCCGTGGAGGACCAAG 384
361 CGGACGTTCCGTGGAGGACCAAG 384
RESULT 3
ADP45590
ID ADP45590 standard; cDNA; 717 BP.
XX
AC
XX
XX
DT 09-SEP-2004 (first entry)
XX
DE Mouse binding molecule 11C7 light chain cDNA SEQ ID NO:44.
XX
XX binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
KW nerve repair; neuroprotective; gene therapy;
KW central nervous system injury; CNS injury; neurodegenerative disorder;
KW mouse; gene; ss.
XX
OS Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..717
FT /*tag= a
FT /product= "binding molecule 11C7 light chain"
XX
XX
PN WO2004052932-A2.
XX
PD 24-JUN-2004.
XX
XX 09-DEC-2003; 2003WO-EP013960.
XX
PR 10-DEC-2002; 2002GB-00028832.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
PA (UYZU-) UNIV ZUERICH.
XX
XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
PI Zurini M;
XX
XX WPI; 2004-468818/44.
XX
XX
PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
XX
XX Example 5; SEQ ID NO 44; 121pp; English.
PS
XX The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes a mouse binding molecule 11C7 light chain, which is used in the exemplification of the present invention.
XX
SQ Sequence 717 BP; 194 A; 176 C; 175 G; 172 T; 0 U; 0 Other;
Query Match 93.6%; Score 370.6; DB 12; Length 717;
Best Local Similarity 96.4%; Pred. No. 6.3e-111;
Matches 379; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 ATGAGTCTGCCCCAGTTCTGTTTCTGTTAGTGTCTGGATTCGGGAACCAACGGTTAT 63
Db |||||
1 ATGAGTCTGCCCCAGTTCTGTTTCTGTTAGTGTCTGGATTCGGGAACCAACGGTTAT 60
QY 64 GTTGTGATGACCCAGACTCCACTCAGTTTGTGCGTTACCATTTGGACCAACGCTCCATC 123
Db |||||
61 GTTCTGTTGACCCAGACTCCTCTCACTTTGTGATAACCAATTTGGACCAACGCTCCATC 120
QY 124 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGATGGAAGACATATTTGAATTGGTTG 183
Db |||||
121 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGATGGAAGACATATTTGAATTGGTTG 180
QY 184 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTCTAAACTGGACTCT 243
Db |||||
181 TTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTCTAAACTGGACTCT 240
QY 244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCAGC 303
Db |||||
241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGGATTTTACACTGAAATCAGC 300
QY 304 AGAATAGAGGCTGAGGATTTGGACTTTTATTATTGTTGGCAAGGTACACATTTTCTCGG 363
Db |||||
301 AGAGTGGAGGCTGAGGATTTGGACTTTTATTATTGTTGGCAAGGTACACATTTTCTCGG 360
QY 364 ACGTTCGGTGGAGGCCACCAAGCTGGAATCAAA 396
Db |||||
361 ACGTTCGGTGGAGGCCACCAAGCTGGAATCAAA 393
RESULT 4
ABN84610
ID ABN84610 standard; cDNA; 420 BP.
XX
AC ABN84610;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen Mab SWLA3 VL coding region.
XX
KW Streptococcus mutans; monoclonal antibody; Mab; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy; gene; ss.
XX
OS Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT CDS 13..417
FT /*tag= a
FT /partial
FT /product= "SWLA3 light chain variable region"
FT /note= "the CDS does not include a stop codon"
XX
PN US2002068066-A1.
XX
XX 06-JUN-2002.
PD
XX 15-JUN-2001; 2001US-00881823.
PF
XX 20-AUG-1999; 99US-00378577.
PR
XX (SHIW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
DR WPI; 2002-565838/60.
DR P-PSDB; ABB79729.
XX
PT Treatment and prevention of dental caries in mammals, in particular

XX Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic; gene; ss.

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 1..717

FT /*tag= a

FT /product= "Humanised 3D6 antibody light chain"

FT /partial

FT /note= "the CDS does not include a stop codon"

FT sig_peptide 1..60

FT /*tag= b

FT mat_peptide 61..717

FT /*tag= c

XX WO200288306-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011853.

XX 30-APR-2001; 2001US-0287539P.

XX (ELIL) LILLY & CO ELI.

XX Tsurushita N, Vasquez M;

XX WPI; 2003-183835/18.

XX P-PSDB; ABP58274.

XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.

XX Claim 15; Page 12-13; 54pp; English.

XX The present sequence is that of cDNA encoding a preferred light chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 27-OCT-2003 to standardise OS field)

XX Sequence 717 BP; 182 A; 185 C; 185 G; 165 T; 0 U; 0 Other;

SQ Query Match 91.9%; Score 364; DB 8; Length 717; Best Local Similarity 94.9%; Pred. No. 9.3e-109; Matches 376; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGGGAAACCAACGGT 60

Db 1 ATGATGAGTCCTGCCAGTTCCTGTTTCTGTAGTGTCTGGATTGGGAAACCAACGGT 60

QY 61 TATGTTGTGATGACCCAGACTCCCACTCACTTTGTCTGGTTACCATTTGGACACAGCTCC 120

Db 61 GATGTTGTGATGACCCAGTCTCCACTCTCTTGCCTGTGTACCTGGGACACAGCTCC 120

QY 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTATGAGAAAGACATATTTGAATTGG 180

Db 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTATGAGAAAGACATATTTGAATTGG 180

QY 181 TTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTTAATCTATCTGGTGTCTAAACTGGAC 240

Db 181 TTGCAACAGCGCCAGGCCAGTCTCCAAAGCGCCTTAATCTATCTGGTGTCTAAACTGGAC 240

QY 241 TCTGGAGTCCCTGACAGGTTCTCTGGCAGTGGATCAGGGACAGATTTTACACTGAAAAATC 300

Db 241 TCTGGAGTCCCTGACAGGTTCTCTGGCAGTGGATCAGGGACAGATTTTACACTGAAAAATC 300

QY 301 AGCAGATAGAGGCTGAGGATTTGGGACTTTATTTATTTGCTGGCAAGGTACACATTTTCCT 360

Db 301 AGCAGATCGAGGCTGAGGATTTGGGAGTTTATTTATTTGCTGGCAAGGTACACATTTTCCT 360

QY 361 CGGACGTTTCGGTGGAGGCACCAAGCTGGAATCAAA 396

Db 361 CGGACGTTTCGGTGGAGGCACCAAGGTGGAATCAAA 396

RESULT 7

ABZ24634

ID ABZ24634 standard; DNA; 1953 BP.

XX AC ABZ24634;

XX 27-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX Humanised 3D6 antibody light chain gene.

DE Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic; gene; ds.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 12..1088

FT /*tag= a

FT /product= "Humanised antibody light chain"

FT /note= "includes an intron"

FT exon 12..408

FT /*tag= b

FT intron 409..765

FT /*tag= c

FT exon 766..1088

FT /*tag= d

FT polyA_signal 1261..1266

FT /*tag= e

XX WO200288306-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011853.

XX 30-APR-2001; 2001US-0287539P.

XX (ELIL) LILLY & CO ELI.

XX Tsurushita N, Vasquez M;

XX WPI; 2003-183835/18.

XX P-PSDB; ABP58274.

XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral

Query Match 91.1%; Score 360.8; DB 2; Length 426;
Best Local Similarity 94.4%; Pred. No. 8.3e-108;
Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTCTGCGCCAGTTCCTGTTCTGTAGTCTCTGGATTCGGGAACCAACCGGT 60
Db 31 ATGATGAGTCTCTGCGCCAGTTCCTGTTCTGTAGTCTCTGGATTCGGGAACCAACCGGT 90
QY 61 TATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCAATGGACAACCAAGCTCC 120
Db 91 GATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCAATGGACAACCAAGCTCC 150
QY 121 ATCTCTTGCAGTCAAGTCAGAGCCTCTTATAGATAGTGAAGACATATTTGAATTGG 180
Db 151 TTCTCTTGCAGTCAAGTCAGAGCCTCTTATAGATAGTGAAGACATATTTGAATTGG 210
QY 181 TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGCTGTCTAAACTGGAC 240
Db 211 TTCTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGCTGTCTAAACTGGAC 270
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 300
Db 271 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 330
QY 301 ACCAGATAGAGGCTGAGGATTTGGGACTTTATATTATGCTGGCAAGGTACACATTTTCCT 360
Db 331 ACCAGATGGAGGCTGAGGATTTGGGAGTTTATATTATGCTGGCAAGGTTCACATTTTCCG 390
QY 361 CGGACGTTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396
Db 391 ATCACGTTTCGGTGGAGGCCACCAAGCTAGAACTGAGA 426

RESULT 11
AAQ12019
ID AAQ12019 standard; DNA; 426 BP.
XX
AC AAQ12019;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1991 (first entry)
XX
XX Sequence encoding mouse Mab 4D12 L chain V region.
DE
DE HIV-1; chimera; ds.
KW
XX
XX Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 31..426
FT /*tag= a
XX
XX WO9107494-A.
PN
XX
XX 30-MAY-1991.
PD
XX
XX 13-NOV-1989; 89US-004333703.
PF
XX
XX 13-NOV-1989; 89US-004333703.
PR
XX
XX (XOMA) XOMA CORP.
PA (GREG) GREEN CROSS CORP.
PA (ZOMA-) ZOMA CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX
XX WPI; 1991-178106/24.
DR P-PSDB; AAR12239.
DR
XX
XX New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
PT
XX
XX Disclosure; Fig 18; 108pp; English.
PS

XX The mouse VL gene product may be used to produce chimeric mouse- human
CC Abs against HIV-1 comprising human Ig constant regions and murine
CC variable regions. These novel sequence are useful in treatment, diagnosis
CC and prophylaxis of HIV infections, and may be produced by a bacterial,
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 426 BP; 100 A; 99 C; 105 G; 122 T; 0 U; 0 Other;
Query Match 91.1%; Score 360.8; DB 2; Length 426;
Best Local Similarity 94.4%; Pred. No. 8.3e-108;
Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTCTGCGCCAGTTCCTGTTCTGTAGTCTCTGGATTCGGGAACCAACCGGT 60
Db 31 ATGATGAGTCTCTGCGCCAGTTCCTGTTCTGTAGTCTCTGGATTCGGGAACCAACCGGT 90
QY 61 TATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCAATGGACAACCAAGCTCC 120
Db 91 GATGTTGTGATGACCCAGACTCCACTCCTTTGTGCGTTACCAATGGACAACCAAGCTCC 150
QY 121 ATCTCTTGCAGTCAAGTCAGAGCCTCTTATAGATAGTGAAGACATATTTGAATTGG 180
Db 151 TTCTCTTGCAGTCAAGTCAGAGCCTCTTATAGATAGTGAAGACATATTTGAATTGG 210
QY 181 TTGTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGCTGTCTAAACTGGAC 240
Db 211 TTCTTACAGAGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGCTGTCTAAACTGGAC 270
QY 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAAATC 300
Db 271 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 330
QY 301 AGCAGATAGAGCTGAGGATTTGGGACTTTATATTATGCTGGCAAGGTACACATTTTCCT 360
Db 331 AGCAGATGGAGGCTGAGGATTTGGGAGTTTATATTATGCTGGCAAGGTTCACATTTTCCG 390
QY 361 CGGACGTTTCGGTGGAGGCCACCAAGCTGGAAATCAAA 396
Db 391 ATCACGTTTCGGTGGAGGCCACCAAGCTAGAACTGAGA 426

RESULT 12
ABX16570
ID ABX16570 standard; DNA; 729 BP.
XX
AC ABX16570;
XX
DT 22-APR-2003 (first entry)
XX
XX Mouse DNA encoding antibody 3D8 light chain variable region.
DE
XX ds; T-cell receptor; gene; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; heavy chain variable region; mouse.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 15..410
FT /*tag= a
FT /product= ""3D8 light chain variable region""
FT /partial
FT /note= "No stop codon shown"
XX
XX US2002132983-A1.
PN
XX
XX 19-SEP-2002.
PD
XX
XX 10-DEC-2001; 2001US-00006773.
PF

XX 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX (JUNG/) JUNGHANS R P.
PA Junghans RP;
XX WPI; 2003-208946/20.
DR P-PSDB; ABG74244.
XX New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX Claim 2; Fig 4B; 35pp; English.
XX The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC encodes the mouse antibody 3D8 light chain variable region
XX
SQ Sequence 729 BP; 203 A; 177 C; 172 G; 177 T; 0 U; 0 Other;

Query Match 90.9%; Score 359.8; DB 8; Length 729;
Best Local Similarity 94.4%; Pred. No. 2.2e-107;
Matches 373; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 2 TGATGAGTCTGCCCCAGTCTCTGTTCTGTGTAGTCTGTGGATTCCGGAAACCAACGGTT 61
DB 13 TGATGAGTCTGCCCCAGTCTCTGTTCTGTGTAGTCTGTGGATTCCGGAAACCAACGGTG 72
QY 62 ATGTTGTGATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACACCAAGCTCCA 121
DB 73 ATGTTGTAATGACCCAGACTCCACTCATTGTCGGTTACCATTTGGACACCAAGCTCTA 132
QY 122 TCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTATGATGGAAGACATATTTGAATTGGT 181
DB 133 TCTCTTGAAGTCAAGTCAGAGCTCTTATATAGTAATGGAAGAAACCTATTGGAATTGGT 192
QY 182 TGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTAAACTGGACT 241
DB 193 TATTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGTTGTTAAACTGGACT 252
QY 242 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCA 301
DB 253 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGACAGATTTTACACTGAAATCA 312
QY 302 GCAGATAGAGGCTGAGGATTTGGGACTTTTATTATGCTGGCAAGGTACACATTTTCCTC 361
DB 313 GCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCGTGCAGAGGTACACATTTTCCTC 372
QY 362 GGACGTTGCTGGAGGCCAAGCTGGAAATCAAA 396
DB 373 ACACGTTGGAGGGGGGACCAAGCTGGAAATCAAA 407

RESULT 13
AAQ25691
ID AAQ25691 standard; cDNA; 737 BP.
XX
AC AAQ25691;

XX 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)
XX Sequence of the chimeric kappa chain cDNA (lgkv) contained in pTB1427.
XX Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy; ss.
XX Synthetic.
XX Key Location/Qualifiers
FT sig_peptide 12..71
FT /tag= a
FT /label= leader
FT CDS 72..410
FT /tag= b
FT /product= "V-kappa"
FT 134..731
FT /tag= c
FT /product= "C-kappa"
XX EP491351-A2.
XX 24-JUN-1992.
XX 17-DEC-1991; 91EP-00121591.
XX 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Iwasa S, Tada H, Watanabe T;
PI WPI; 1992-209528/26.
DR P-PSDB; AAR24811.
XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX Example; Fig 9; 87pp; English.
XX Poly(A) + RNA was prepd. from the anti-fibrin chimeric AB-producing
CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa
CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand
CC cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An
CC amplified DNA fragment of about 0.33kb was isolated and used to create a
CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the
CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa
CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)
CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first
CC stand synthesis and the 5'mv-kappa and 3'mv-kappa primers for the PCR, an
CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a
CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a
CC primer for first strand synthesis and the 5'S-kappa and 3'L-kappa
CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v; V-
CC kappa-FIB) were isolated and used to construct respectively plasmids
CC pTB1391, pTB1392, and pTB1393. L-kappa, V-kappa and C-kappa were joined
CC together to give a plasmid, pTB1427, contg. the whole length of the
CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 737 BP; 186 A; 187 C; 189 G; 175 T; 0 U; 0 Other;
Query Match 87.1%; Score 344.8; DB 2; Length 737;
Best Local Similarity 91.9%; Pred. No. 1.9e-102;
Matches 364; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTCTCTGATTCGGAAACCAACGGT 60
DB 12 ATGATGAGTCTGCCAGTTCCTGTTTCTGTGTAGTCTCTGATTCGGAAACCGGTGGT 71

RESULT 15
ADQ89317
ID ADQ89317 standard; DNA; 426 BP.
XX AC
XX ADQ89317;
XX AC
DT 21-OCT-2004 (first entry)
XX DE
XX Mouse immunoglobulin DNA #1.
XX KW Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
XX KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
XX KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
XX KW anti-HIV; virucide; antiarteriosclerotic; gene; ds.
XX OS Mus musculus.
XX OS
XX PN US2004151721-A1.
XX PN
XX PD 05-AUG-2004.
XX PD
XX PP 10-DEC-2003; 2003US-00733563.
XX PP
XX PR 19-OCT-2001; 2001US-0350166P.
XX PR
XX PR 26-JUN-2002; 2002US-0392364P.
XX PR
XX PR 17-OCT-2002; 2002US-00272899.
XX PR
XX PA (OKEE/) O'KEEFE T.
XX PA (PONA/) PONATH P.
XX PI
XX PI O'keefe T, Ponath P;
XX PI
XX DR WPI; 2004-580175/56.
XX DR P-PSDB; ADQ89324.
XX DR
XX PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
XX PT useful for diagnosing and/or treating inflammatory or autoimmune
XX PT diseases, and HIV infection.
XX PT
XX PS Disclosure; SEQ ID NO 95; 128pp; English.
XX PS
XX CC The invention relates to humanised immunoglobulin heavy and light chains
XX CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
XX CC immunoglobulin or its antigen binding fragment comprising the chains. The
XX CC humanised immunoglobulin or its antigen binding fragment preferably
XX CC comprises two heavy chains and two light chains. The humanised
XX CC immunoglobulin and its heavy and light chains are useful for the
XX CC diagnosis, prevention and/or treatment of diseases or conditions
XX CC associated with aberrant expression or activity of the CCR2 polypeptide,
XX CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
XX CC infection and atherosclerosis. This sequence represents DNA encoding a
XX CC mouse immunoglobulin protein of the invention.
XX CC
SQ Sequence 426 BP; 104 A; 97 C; 114 G; 111 T; 0 U; 0 Other;
Query Match 84.7%; Score 335.4; DB 13; Length 426;
Best Local Similarity 94.3%; Pred. No. 1.8e-99;
Matches 348; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 28 CTGTTAGTCTCTGGATTCCGGGAAACCAACCGTTATGTTGTGATGACCCAGACTCCACTC 87
Db 19 CTGTTGGTGCTCTGGATTCCGGGAGACAATCGCGATGTTGTGATGACCCAGACTCCACTC 78
Qy 88 ACTTTGTCGGTTACCATTTGGACAAACAGCCCTCCATCTCTTGCAGTCAAGTCAGAGCCCTC 147
Db 79 ACTTTGTCGGTTACCGTTGGACACCAGCCCTCCATCTCTTGCAGTCAAGTCAGAGCCCTC 138
Qy 148 TTAGATAGTATGAGAAAGACATATTGAAATTGGTTGTTACAGAGGCCAGCCAGTCTCCA 207
Db 139 TTAGATAGTATGAGAAAGACATTTTGAATTGGTTGTTACAGAGGCCAGCCAGTCTCCA 198
Qy 208 AAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGC 267

Db 199 AAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGC 258
Qy 268 AGTGGATCAGGACAGATTTTACACTGAAAATCAGCAGAAATAGAGGCTGAGGATTTGGGA 327
Db 259 AGTGGATCAGGACAGATTTTACACTGAAAATCAGCAGAAATAGAGGCTGAGGATTTGGGA 318
Qy 328 CTTTATTATTGCTGGCAAGGTACACATTTTCTCGGACGTTTCGGTGGAGGCCACCAAGCTG 387
Db 319 GTTTATTATTGCTGGCAAGGTACACATTTTCTCGGATACACGTTTCGGAGGGGGACCAAGCTG 378
Qy 388 GAAATCAAA 396
Db 379 GAAATAAAA 387
Search completed: September 26, 2005, 05:09:03
Job time : 397 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2005, 05:48:07 ; Search time 90 Seconds
(without alignments)
751.049 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLMWIRETNG.....CWQGTFFPRTFGGPKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	73.8	239	2 Q8TCD0	Q8tcd0 homo sapien
2	508	73.4	133	1 KV2F_HUMAN	P06310 homo sapien
3	471	68.1	239	2 Q8NEK0	Q8nek0 homo sapien
4	471	68.1	239	2 Q6P491	Q6p491 homo sapien
5	444.5	64.2	114	2 Q9UL80	Q9ul80 homo sapien
6	441.5	63.8	240	2 Q6PIH6	Q6pih6 homo sapien
7	434	62.7	113	1 KV2G_MOUSE	P01631 mus musculus
8	430	62.1	219	2 Q65ZC0	Q65zc0 mus musculus
9	425	61.4	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
10	417	60.3	117	1 KV2E_HUMAN	P06309 homo sapien
11	415	60.0	113	1 KV2D_HUMAN	P01617 homo sapien
12	414.5	59.9	115	1 KV2A_HUMAN	P01614 homo sapien
13	414	59.8	113	1 KV2B_HUMAN	P01615 homo sapien
14	389.5	56.3	112	1 KV2C_HUMAN	P01616 homo sapien
15	388	56.1	113	1 KV2F_MOUSE	P01630 mus musculus
16	386	55.8	129	1 KV3L_HUMAN	P18135 homo sapien
17	381	55.1	112	2 Q6LEM8	Q6lem8 mus musculus
18	380.5	55.0	134	1 KV4C_HUMAN	P06314 homo sapien
19	380	54.9	113	1 KV2E_MOUSE	P03976 mus musculus
20	377.5	54.6	236	2 Q6PIL8	Q6pil8 homo sapien
21	376	54.3	235	2 Q6GMV9	Q6gmv9 homo sapien
22	374	54.0	112	1 KV2D_MOUSE	P01629 mus musculus
23	374	54.0	120	1 KV2B_MOUSE	P01627 mus musculus
24	373.5	54.0	131	1 KV3I_MOUSE	P01661 mus musculus
25	373	53.9	113	1 KV2C_MOUSE	P01628 mus musculus
26	373	53.9	129	1 KV3M_HUMAN	P18136 homo sapien
27	373	53.9	133	1 KV4B_HUMAN	P06313 homo sapien
28	369	53.3	112	1 KV2A_MOUSE	P01626 mus musculus
29	368.5	53.3	236	2 Q6P5S8	Q6p5s8 homo sapien
30	363.5	52.5	108	1 KV1_CANFA	P01618 canis famil
31	362.5	52.4	236	2 Q7TS98	Q7ts98 mus musculus

RESULT 1
Q8TCD0 ID Q8TCD0 PRELIMINARY; PRT; 239 AA.

AC Q8TCD0;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; --
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.

ALIGNMENTS


```
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical
CC with the Bence Jones protein isolated from the same patient.
CC -!- MISCELLANEOUS: This protein was isolated from the urine of a
CC patient with plasma cell dyscrasia and amyloidosis.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
DR PIR; A90370; K2HUTW.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-4.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 60.0%; Score 415; DB 1; Length 113;
Best Local Similarity 71.2%; Pred. No. 2.3e-32;
Matches 79; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 22 VVMTQPTLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 IVMTQSPISLPVTPGEPASISCRSSQSLHSDGFDYLNWYLNKPGQSPZLLIYALSNRAS 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 82 GVPDRFTGSGSGTDFTLKISRVEADGLGYCQGTTHFPRTFGGKLEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GVPDRFSGSGSGTDFTLKISRVEADGVVYCMZALQAPITFGQGRLEIK 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
KV2A HUMAN
ID KV2A HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
```

```
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilechmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilechmann N.;
RT "Molecular basis of antibody formation."
RL Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; B91639; K2HUCM.
DR HSSP; P01751; INQB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DISULFID 24 95 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 59.9%; Score 414.5; DB 1; Length 115;
Best Local Similarity 72.3%; Pred. No. 2.6e-32;
Matches 81; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 22 VVMTQPTLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 IVMTQPTLSLPVTPGEPASISCRSSQSLDSDGNTYLNWYLNKAGQSPQLIYTLSTRA 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 SGVPDRFTGSGSGTDFTLKISRVEADGLGYCQGTTHFPRTFGGKLEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGVPDRFSGSGSGTDFTLKISRVEADGVVYCMQRLIPIYTFGQGTLEIR 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
KV2B HUMAN
ID KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
RT with specificity for phosphorylcholine."
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin that binds phosphorylcholine.
DR PIR; A01886; K2HUFR.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
```

```
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match
Best Local Similarity 59.8%; Score 414; DB 1; Length 113;
Matches 77; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 22 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQSPLFLPVTLPGEPAISQCRSSQSLVYRBGTYLWYLRQKPGQPELLIYLSYRDS 61

QY 82 GVPDRFTGSGSGTDFTLKISRIEAEDGLIYCWQGTFFPRFTGGGKLEIK 132
Db 62 GVPDRFSDSGSGTDFTLKITRVAEDGVYVYCMQATZSPYTFGGTKLZIK 112

RESULT 14
KV2C HUMAN
ID KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 119I.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match
Best Local Similarity 56.3%; Score 389.5; DB 1; Length 112;
Matches 77; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
```

```
Best Local Similarity 63.1%; Pred. No. 6.6e-30;
Matches 70; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

QY 22 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IVLTQSPLSLPVTLPGEPAISQCRSSQSLDZSGB-YLDWTLYZKPGSPZLLIYLSNRAS 60

QY 82 GVPDRFTGSGSGTDFTLKISRIEAEDGLIYCWQGTFFPRFTGGGKLEIK 132
Db 61 GVPDRFSGSGSGTBTFLKISRVAZBVGYYVCMQALQTLPTLTFGGGTNVEIK 111

RESULT 15
KV2F MOUSE
ID KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVMS7S.
DR HSSP; Q99M37; 119I.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match
Best Local Similarity 56.1%; Score 388; DB 1; Length 113;
Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 22 VVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 IVMTQTAPSLVTPGESVSIKSRSSKSLHSGNGLYLYWFLQRPQCPQLLIYRMSNLAS 61

QY 82 GVPDRFTGSGSGTDFTLKISRIEAEDGLIYCWQGTFFPRFTGGGKLEIK 132
Db 62 GVPDRFSGSGSGTAFTLRISRVEAEDGVYVYCMQREYPTFTGGGKLEIK 112

Search completed: September 26, 2005, 07:17:55
Job time : 91 secs
```

This Page Blank (uspto)